

## Sequence Listing

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 Botstein, David  
 Desnoyers, Luc  
 Eaton, Dan  
 Ferrara, Napoleon  
 Filvaroff, Ellen  
 Fong, Sherman  
 Gao, Wei-Qiang  
 Gerber, Hanspeter  
 Gerritsen, Mary E.  
 Goddard, Audrey  
 Godowski, Paul J.  
 Grimaldi, J. Christopher  
 Gurney, Austin L.  
 Hillan, Kenneth J  
 Kljavin, Ivar J.  
 Kuo, Sophia S.  
 Napier, Mary A.  
 Pan, James;  
 Paoni, Nicholas F.  
 Roy, Margaret Ann  
 Shelton, David L.  
 Stewart, Timothy A.  
 Tumas, Daniel  
 Williams, P. Mickey  
 Wood, William I.

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 His Ser His Leu Glu Cys Arg Glu Pro Leu Leu Ile Pro Ile Leu  
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 Ser Leu Tyr Met Gly Ala Leu Val Arg Cys Thr Thr Leu Cys Leu  
 200 205 210

Gly Tyr Tyr Lys Asn Ile His Asp Ile	Ile Pro Asp Arg Ser Gly	215	220	225
Pro Glu Leu Gly Gly Asp Ala Thr Ile	Arg Lys Met Leu Ser Phe	230	235	240
Trp Trp Pro Leu Ala Leu Ile Leu Ala	Thr Gln Arg Ile Ser Arg	245	250	255
Pro Ile Val Asn Leu Phe Val Ser Arg	Asp Leu Gly Gly Ser Ser	260	265	270
Ala Ala Thr Glu Ala Val Ala Ile Leu	Thr Ala Thr Tyr Pro Val	275	280	285
Gly His Met Pro Tyr Gly Trp Leu Thr	Glu Ile Arg Ala Val Tyr	290	295	300
Pro Ala Phe Asp Lys Asn Asn Pro Ser	Asn Lys Leu Val Ser Thr	305	310	315
Ser Asn Thr Val Thr Ala Ala His Ile	Lys Lys Phe Thr Phe Val	320	325	330
Cys Met Ala Leu Ser Leu Thr Leu Cys	Phe Val Met Phe Trp Thr	335	340	345
Pro Asn Val Ser Glu Lys Ile Leu Ile	Asp Ile Ile Gly Val Asp	350	355	360
Phe Ala Phe Ala Glu Leu Cys Val Val	Pro Leu Arg Ile Phe Ser	365	370	375
Phe Phe Pro Val Pro Val Thr Val Arg	Ala His Leu Thr Gly Trp	380	385	390
Leu Met Thr Leu Lys Lys Thr Phe Val	Leu Ala Pro Ser Ser Val	395	400	405
Leu Arg Ile Ile Val Leu Ile Ala Ser	Leu Val Val Leu Pro Tyr	410	415	420
Leu Gly Val His Gly Ala Thr Leu Gly	Val Gly Ser Leu Leu Ala	425	430	435
Gly Phe Val Gly Glu Ser Thr Met Val	Ala Ile Ala Ala Cys Tyr	440	445	450
Val Tyr Arg Lys Gln Lys Lys Lys Met	Glu Asn Glu Ser Ala Thr	455	460	465
Glu Gly Glu Asp Ser Ala Met Thr Asp	Met Pro Pro Thr Glu Glu	470	475	480
Val Thr Asp Ile Val Glu Met Arg Glu	Glu Asn Glu	485	490	

<210> 8  
<211> 535  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 33, 66, 96, 387  
<223> unknown base

<400> 8  
cctgacagaa gtgccccgga gctgggggag atncaacatt aagaagatgc 50  
tgagcttctg gtgccttttg gctctaattc tggccacaca gagaancagt 100  
cggcctattg tcaacctctt tgtttcccg gaccttggtg gcagttctgc 150  
agccacagag gcagtgggca ttttgacagc cacataccct gtgggtcaca 200  
tgccatacgg ctggttgacg gaaatccgtg ctgtgtatcc tgctttogac 250  
aagaataacc ccagcaaca actggtgagc acgagcaaca cagtcacggc 300  
ggccacatc aagaagttca ccttcgtctg catggctctg tcaactcacgc 350  
tctgtttcgt gatgttttg acaccaacg tgtctgngaa aatcttgata 400  
gacatcatcg gagtggactt tgcctttgca gaactctgtg ttgttccttt 450  
gcggatcttc tccttcttcc cagttccagt cacagtgagg gcgcattctca 500  
ccgggtggct gatgacactg aagaaaacct tcgtc 535

<210> 9  
<211> 434  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 32, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 228, 273,  
293, 296, 305, 336, 358, 361  
<223> unknown base

<400> 9  
tgacggaatc ccgggctggg tctcctggtt tngacaagat aaacccccag 50  
caanaaattg gggagcaggg caaaacagtn acgggcagcc cacatcaaga 100  
agttcacctt ngtttgnatg gntctgtcaa ctcacgctnt gtttcgtgat 150  
gttttgagca cccaaagtgt ttgagaaaat tttgatagac atnatcggag 200  
tggantttgc ctttgacagaa ntttgnntg ttcctttgcg gattttctcc 250  
tttttccag ttccagtcac agngagggcg catctcaccg ggnggntgat 300

gacantgaag aaaacctttg tccttgcccc cagctntttg gtgcggatca 350  
ttgtcctnat ngccagcctt gtggtcctac cctacctggg ggtgcacggt 400  
gcgaccctgg gcgtgggttc cctcctggcg ggca 434

<210> 10  
<211> 154  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 33, 49, 68, 83, 90, 98, 119  
<223> unknown base

<400> 10  
tattcccagt tccggtcacg gggagggcgc atntcaccgg gtggctgang 50  
acactgaaga aaaccttngt ccttgcccc agntttgtgn tgcggatnat 100  
cgctctcatc gccagcctng tggctctacc ctacctgggg gtgcacggtg 150  
agac 154

<210> 11  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 11  
ctgatccggt tcttggtgcc cctg 24

<210> 12  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 12  
gctctgtcac tcacgctc 18

<210> 13  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 13  
tcattctctc cctctccc 18

<210> 14  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 14  
ccttcgcgcca cggagttc 18

<210> 15  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 15  
ggcaaagtcc actccgatga tgtc 24

<210> 16  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 16  
gcctgctgtg gtcacaggtc tccg 24

<210> 17  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 17  
tcggggagca ggccttgaac cggggcattg ctgctgtcaa ggagg 45

<210> 18  
<211> 1901  
<212> DNA  
<213> Homo sapiens

<400> 18  
gccccgcgcc cggcgccggg cgcccggaagc cgggagccac cgccatgggg 50  
gcctgcctgg gagcctgctc cctgctcagc tgcgcgtcct gcctctgcgg 100  
ctctgcccc ctcacacctgt gcagctgctg ccccgccagc cgcaactcca 150



ccgtgagccg cctcatcttc acgttcttcc tcttcctggg ggtgctggtg 200  
tccatcatta tgctgagccc gggcgtggag agtcagctct acaagctgcc 250  
ctgggtgtgt gaggaggggg ccgggatccc caccgtcctg cagggccaca 300  
tcgactgtgg ctccctgctt ggctaccgag ctgtctaccg catgtgcttc 350  
gccacggcgg ccttcttctt cttctttttc accctgctca tgctctgcgt 400  
gagcagcagc cgggaccccc gggtgccat ccagaatggg ttttggttct 450  
ttaagtctct gatcctggtg ggctcaccg tgggtgcctt ctacatccct 500  
gacggctcct tcaccaacat ctggttctac ttcggcgtcg tgggtcctt 550  
cctcttcate ctcatccagc tgggtgctgt catcgacttt gcgcactcct 600  
ggaaccagcg gtggctgggc aaggccgagg agtgcgattc ccgtgcctgg 650  
tacgcaggcc tcttcttctt cactctctc ttctacttgc tgcgatcgc 700  
ggccgtggcg ctgatgttca tgtactacac tgagcccagc ggctgccacg 750  
agggcaaggt cttcatcagc ctcaacctca cttctgtgt ctgcgtgtcc 800  
atcgtgctg tctgccccaa ggtccaggac gccagccca actcgggtct 850  
gctgcaggcc tcggtcatca ccctctacac catgtttgtc acctggtcag 900  
ccctatccag tatccctgaa cagaaatgca accccattt gccaacccag 950  
ctgggcaacg agacagttgt ggcaggcccc gagggctatg agaccagtg 1000  
gtgggatgcc ccgagcattg tgggcctcat catcttctc ctgtgcaccc 1050  
tcttcatcag tctgcgtcc tcagaccacc ggcaggtgaa cagcctgatg 1100  
cagaccgagg agtcccacc tatgctagac gccacacagc agcagcagca 1150  
gcaggtggca gcctgtgagg gccgggcctt tgacaacgag caggacggcg 1200  
tcacctacag ctactcttc ttccacttct gcctggtgct ggctcactg 1250  
cacgtcatga tgacgtcac caactggtac aagcccgggtg agaccggaa 1300  
gatgatcagc acgtggaccg ccgtgtgggt gaagatctgt gccagctggg 1350  
cagggtgct cctctacctg tggaccctgg tagccccact cctcctgcgc 1400  
aaccgcgact tcagctgagg cagcctcaca gcctgccatc tgggtgcctcc 1450  
tgccacctgg tgctctcgg ctcggtgaca gccaacctgc cccctcccca 1500  
caccaatcag ccaggctgag ccccccaccc tgccccagct ccaggacctg 1550  
ccctgagcc gggccttcta gtcgtagtgc cttcagggtc cgaggagcat 1600

caggctcctg cagagcccca tccccccgcc acaccacac ggtggagctg 1650  
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 agggctccct tgtcctcagg ctccacggga gcggggctgc tggagagagc 1750  
 ggggaactcc caccacagtg gggcatccgg cactgaagcc ctggtgttcc 1800  
 tggtcacgtc ccccagggga cctgcccccc ttctgggact tcgtgcctta 1850  
 ctgagtctct aagacttttt ctaataaaca agccagtgcg tgtaaaaaaa 1900  
 a 1901

<210> 19  
 <211> 457  
 <212> PRT  
 <213> Homo sapiens

<400> 19  
 Met Gly Ala Cys Leu Gly Ala Cys Ser Leu Leu Ser Cys Ala Ser  
 1 5 10 15  
 Cys Leu Cys Gly Ser Ala Pro Cys Ile Leu Cys Ser Cys Cys Pro  
 20 25 30  
 Ala Ser Arg Asn Ser Thr Val Ser Arg Leu Ile Phe Thr Phe Phe  
 35 40 45  
 Leu Phe Leu Gly Val Leu Val Ser Ile Ile Met Leu Ser Pro Gly  
 50 55 60  
 Val Glu Ser Gln Leu Tyr Lys Leu Pro Trp Val Cys Glu Glu Gly  
 65 70 75  
 Ala Gly Ile Pro Thr Val Leu Gln Gly His Ile Asp Cys Gly Ser  
 80 85 90  
 Leu Leu Gly Tyr Arg Ala Val Tyr Arg Met Cys Phe Ala Thr Ala  
 95 100 105  
 Ala Phe Phe Phe Phe Phe Phe Thr Leu Leu Met Leu Cys Val Ser  
 110 115 120  
 Ser Ser Arg Asp Pro Arg Ala Ala Ile Gln Asn Gly Phe Trp Phe  
 125 130 135  
 Phe Lys Phe Leu Ile Leu Val Gly Leu Thr Val Gly Ala Phe Tyr  
 140 145 150  
 Ile Pro Asp Gly Ser Phe Thr Asn Ile Trp Phe Tyr Phe Gly Val  
 155 160 165  
 Val Gly Ser Phe Leu Phe Ile Leu Ile Gln Leu Val Leu Leu Ile  
 170 175 180

Asp Phe Ala His Ser Trp Asn Gln Arg	Trp Leu Gly Lys Ala Glu	185	190	195
Glu Cys Asp Ser Arg Ala Trp Tyr Ala	Gly Leu Phe Phe Phe Thr	200	205	210
Leu Leu Phe Tyr Leu Leu Ser Ile Ala	Ala Val Ala Leu Met Phe	215	220	225
Met Tyr Tyr Thr Glu Pro Ser Gly Cys	His Glu Gly Lys Val Phe	230	235	240
Ile Ser Leu Asn Leu Thr Phe Cys Val	Cys Val Ser Ile Ala Ala	245	250	255
Val Leu Pro Lys Val Gln Asp Ala Gln	Pro Asn Ser Gly Leu Leu	260	265	270
Gln Ala Ser Val Ile Thr Leu Tyr Thr	Met Phe Val Thr Trp Ser	275	280	285
Ala Leu Ser Ser Ile Pro Glu Gln Lys	Cys Asn Pro His Leu Pro	290	295	300
Thr Gln Leu Gly Asn Glu Thr Val Val	Ala Gly Pro Glu Gly Tyr	305	310	315
Glu Thr Gln Trp Trp Asp Ala Pro Ser	Ile Val Gly Leu Ile Ile	320	325	330
Phe Leu Leu Cys Thr Leu Phe Ile Ser	Leu Arg Ser Ser Asp His	335	340	345
Arg Gln Val Asn Ser Leu Met Gln Thr	Glu Glu Cys Pro Pro Met	350	355	360
Leu Asp Ala Thr Gln Gln Gln Gln Gln	Gln Val Ala Ala Cys Glu	365	370	375
Gly Arg Ala Phe Asp Asn Glu Gln Asp	Gly Val Thr Tyr Ser Tyr	380	385	390
Ser Phe Phe His Phe Cys Leu Val Leu	Ala Ser Leu His Val Met	395	400	405
Met Thr Leu Thr Asn Trp Tyr Lys Pro	Gly Glu Thr Arg Lys Met	410	415	420
Ile Ser Thr Trp Thr Ala Val Trp Val	Lys Ile Cys Ala Ser Trp	425	430	435
Ala Gly Leu Leu Leu Tyr Leu Trp Thr	Leu Val Ala Pro Leu Leu	440	445	450
Leu Arg Asn Arg Asp Phe Ser		455		

<210> 20  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 20  
gccgcctcat cttcacgttc ttcc 24

<210> 21  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 21  
tcatccagct ggtgctgctc 20

<210> 22  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 22  
cttctttccac ttctgcctgg 20

<210> 23  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 23  
cctgggcaaa aatgcaac 18

<210> 24  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 24  
caggaatgta gaaggcacc acgg 24

<210> 25  
<211> 24

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 25  
tggcacagat cttcacccac acgg 24

<210> 26  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 26  
tgtccatcat tatgctgagc ccgggcgtgg agagtcagct ctacaagctg 50

<210> 27  
<211> 1351  
<212> DNA  
<213> Homo sapiens

<400> 27  
gagcgaggcc ggggactgaa ggtgtgggtg tcgagccctc tggcagaggg 50  
ttaacctggg tcaaatgcac ggattctcac ctcgtacagt tacgctctcc 100  
cgcggcacgt ccgcgaggac ttgaagtcct gagcgctcaa gtttgtccgt 150  
aggtcgagag aaggccatgg aggtgccgcc accggcaccg cggagctttc 200  
tctgtagagc attgtgecta tttccccgag tctttgctgc cgaagctgtg 250  
actgccgatt cggaagtcct tgaggagcgt cagaagcggc ttccctacgt 300  
cccagagccc tattaccgg aatctggatg ggaccgcctc cgggagctgt 350  
ttggcaaaga tgaacagcag agaatttcaa aggaccttgc taatatctgt 400  
aagacggcag ctacagcagg catcattggc tgggtgtatg ggggaatacc 450  
agcttttatt catgctaaac aacaatacat tgagcagagc caggcagaaa 500  
tttatcataa ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca 550  
cgaggcttca ttcgttatgg ctggcgctgg ggttgagaa ctgcagtgtt 600  
tgtgactata ttcaacacag tgaacactag tctgaatgta taccgaaata 650  
aagatgcctt aagccatttt gtaattgcag gagctgtcac gggaagtctt 700  
tttaggataa acgtaggcct gcgtggcctg gtggctgggt gcataattgg 750  
agccttgctg ggcactcctg taggaggcct gctgatggca tttcagaagt 800

acgctggtga gactgttcag gaaagaaaac agaaggatcg aaaggcactc 850  
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 cctccctgag aaaattgaaa gtagtttacg ggaagatgaa cctgagaatg 950  
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 atagataaac aagacaagga ctgaaagtgc tctgaacttg aaactcactg 1050  
 gagagctgaa gggagctgcc atgtccgatg aatgccaca gacaggccac 1100  
 tctttggtca gcctgctgac aaatttaagt gctggtacct gtggtggcag 1150  
 tggttgctc ttgtcttttt cttttctttt taactaagaa tggggctgtt 1200  
 gtactctcac ttacttatc cttaaattta aatacatact tatgtttgta 1250  
 ttaatctatc aatatatgca tacatggata tatccacca cctagatttt 1300  
 aagcagtaaa taaaacattt cgcaaaagat taaagttgaa ttttacagtt 1350  
 t 1351

<210> 28  
 <211> 285  
 <212> PRT  
 <213> Homo sapiens

<400> 28  
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 Leu Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala  
 20 25 30  
 Asp Ser Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Val  
 35 40 45  
 Pro Glu Pro Tyr Tyr Pro Glu Ser Gly Trp Asp Arg Leu Arg Glu  
 50 55 60  
 Leu Phe Gly Lys Asp Glu Gln Gln Arg Ile Ser Lys Asp Leu Ala  
 65 70 75  
 Asn Ile Cys Lys Thr Ala Ala Thr Ala Gly Ile Ile Gly Trp Val  
 80 85 90  
 Tyr Gly Gly Ile Pro Ala Phe Ile His Ala Lys Gln Gln Tyr Ile  
 95 100 105  
 Glu Gln Ser Gln Ala Glu Ile Tyr His Asn Arg Phe Asp Ala Val  
 110 115 120  
 Gln Ser Ala His Arg Ala Ala Thr Arg Gly Phe Ile Arg Tyr Gly  
 125 130 135

Trp	Arg	Trp	Gly	Trp	Arg	Thr	Ala	Val	Phe	Val	Thr	Ile	Phe	Asn	
				140					145					150	
Thr	Val	Asn	Thr	Ser	Leu	Asn	Val	Tyr	Arg	Asn	Lys	Asp	Ala	Leu	
				155					160					165	
Ser	His	Phe	Val	Ile	Ala	Gly	Ala	Val	Thr	Gly	Ser	Leu	Phe	Arg	
				170					175					180	
Ile	Asn	Val	Gly	Leu	Arg	Gly	Leu	Val	Ala	Gly	Gly	Ile	Ile	Gly	
				185					190					195	
Ala	Leu	Leu	Gly	Thr	Pro	Val	Gly	Gly	Leu	Leu	Met	Ala	Phe	Gln	
				200					205					210	
Lys	Tyr	Ala	Gly	Glu	Thr	Val	Gln	Glu	Arg	Lys	Gln	Lys	Asp	Arg	
				215					220					225	
Lys	Ala	Leu	His	Glu	Leu	Lys	Leu	Glu	Glu	Trp	Lys	Gly	Arg	Leu	
				230					235					240	
Gln	Val	Thr	Glu	His	Leu	Pro	Glu	Lys	Ile	Glu	Ser	Ser	Leu	Arg	
				245					250					255	
Glu	Asp	Glu	Pro	Glu	Asn	Asp	Ala	Lys	Lys	Ile	Glu	Ala	Leu	Leu	
				260					265					270	
Asn	Leu	Pro	Arg	Asn	Pro	Ser	Val	Ile	Asp	Lys	Gln	Asp	Lys	Asp	
				275					280					285	

<210> 29  
 <211> 324  
 <212> DNA  
 <213> Homo sapiens

<400> 29  
 cggaagtccc ttgaggagcg tcagaagcgg cttccctacg tcccagagcc 50  
 ctattacccg gaatctggat gggaccgctc cgggagctgt ttggcaaaga 100  
 tgaacagcag agaatttcaa aggaccttgc taatatctgt aagacggcag 150  
 ctacagcagg catcattggc tgggtgtatg ggggaatacc agcttttatt 200  
 catgctaaac aacaatacat tgagcagagc caggcagaaa tttatcataa 250  
 ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca cgaggcttca 300  
 ttcgttcattg gctggcgccg aacc 324

<210> 30  
 <211> 377  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> unsure  
<222> 262, 330, 371  
<223> unknown base

<400> 30  
tcaagtttgt ccgtaggtcg agagaaggcc atggaggtgc cgccaccggc 50  
accgcggagc ttttttctgt agagcattgt gcctatttcc ccgagttttt 100  
gctgccgaag ctgtgactgc cgattcggaa gtccttgagg agcgtcagaa 150  
gcggcttccc tacgtcccag agccctatta cccggaattt ggatgggacc 200  
gcctccggga gctgtttggc aaagatgaac agcagagaat ttcaaaggac 250  
cttgctgata tntgtaagac ggcagctaca gcaggcatca ttggctgggt 300  
gtatggggga ataccagctt ttattcatgn taaacaacaa tacattgagc 350  
agagccaggc agaaatttat nataacc 377

<210> 31  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 31  
tcgtacagtt acgctctccc 20

<210> 32  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 32  
cttgaggagc gtcagaagcg 20

<210> 33  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 33  
ataacgaatg aagcctcgtg 20

<210> 34  
<211> 40  
<212> DNA



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

gctaatatct gtaagacggc agctacagca ggcatcattg 40

<210> 35

<211> 1819

<212> DNA

<213> Homo sapiens

<400> 35

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ccaccacagt ctgctgtgct gcccgcctg ggccaggccc caaaggcaag 100  
gacaaagcag ctgtcaggga acctccgccg gagtcgaatt tacgtgcagc 150  
tgccggcaac cacaggttcc aagatggttt gcgggggctt cgcgtgttcc 200  
aagaactgcc tgtgcgcct caacctgctt tacaccttgg ttagtctgct 250  
gctaattgga attgctgctg ggggcattgg cttcgggctg atttccagtc 300  
tccgagtggc cggcgtggtc attgcagtgg gcatcttctt gttcctgatt 350  
gctttagtgg gtctgattgg agctgtaaaa catcatcagg tgttgctatt 400  
tttttatatg attattctgt tacttgtatt tattgttcag ttttctgtat 450  
cttgcgcttg tttagccctg aaccaggagc aacagggtca gcttctggag 500  
gttggttgga acaatacggc aagtgtcga aatgacatcc agagaaatct 550  
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ggtggcacct ggaatttact gtattcattg tcgggcactg tccactgtgg 1050  
cctttcttag catttttacc tgcagaaaaa ctttgtatgg taccactgtg 1100

ttggttatat ggtgaatctg aacgtacatc tcactggtat aattatatgt 1150  
 agcactgtgc tgtgtagata gttcctactg gaaaaagagt ggaaatttat 1200  
 taaaatcaga aagtatgaga tcctgttatg ttaagggaaa tccaaattcc 1250  
 caattttttt tgggtctttt aggaaagatt gttgtggtaa aaagtgttag 1300  
 tataaaaatg ataatttact tgtagtcttt tatgattaca ccaatgtatt 1350  
 ctagaaatag ttatgtctta ggaaattgtg gtttaatttt tgacttttac 1400  
 aggtaagtgc aaaggagaag tggtttcatg aaatgttcta atgtataata 1450  
 acatttacct tcagcctcca tcagaatgga acgagttttg agtaatcagg 1500  
 aagtatatct atatgatctt gatattgttt tataataatt tgaagtctaa 1550  
 aagactgcat ttttaaacaa gttagtatta atgcgttggc ccacgtagca 1600  
 aaaagatatt tgattatctt aaaaattggt aaataccgtt ttcattgaaat 1650  
 ttctcagtat tgtaacagca acttgtcaaa cctaagcata tttgaatatg 1700  
 atctcccata atttgaaatt gaaatcgtat tgtgtggctc tgtatattct 1750  
 gttaaaaaat taaaggacag aaacctttct ttgtgtatgc atgtttgaat 1800  
 taaaagaaag taatggaag 1819

<210> 36

<211> 204

<212> PRT

<213> Homo sapiens

<400> 36

Met	Val	Cys	Gly	Gly	Phe	Ala	Cys	Ser	Lys	Asn	Cys	Leu	Cys	Ala	1	5	10	15
Leu	Asn	Leu	Leu	Tyr	Thr	Leu	Val	Ser	Leu	Leu	Leu	Ile	Gly	Ile	20	25	30	
Ala	Ala	Trp	Gly	Ile	Gly	Phe	Gly	Leu	Ile	Ser	Ser	Leu	Arg	Val	35	40	45	
Val	Gly	Val	Val	Ile	Ala	Val	Gly	Ile	Phe	Leu	Phe	Leu	Ile	Ala	50	55	60	
Leu	Val	Gly	Leu	Ile	Gly	Ala	Val	Lys	His	His	Gln	Val	Leu	Leu	65	70	75	
Phe	Phe	Tyr	Met	Ile	Ile	Leu	Leu	Leu	Val	Phe	Ile	Val	Gln	Phe	80	85	90	
Ser	Val	Ser	Cys	Ala	Cys	Leu	Ala	Leu	Asn	Gln	Glu	Gln	Gln	Gly	95	100	105	

Gln	Leu	Leu	Glu	Val	Gly	Trp	Asn	Asn	Thr	Ala	Ser	Ala	Arg	Asn	120
				110					115						
Asp	Ile	Gln	Arg	Asn	Leu	Asn	Cys	Cys	Gly	Phe	Arg	Ser	Val	Asn	135
				125					130						
Pro	Asn	Asp	Thr	Cys	Leu	Ala	Ser	Cys	Val	Lys	Ser	Asp	His	Ser	150
				140					145						
Cys	Ser	Pro	Cys	Ala	Pro	Ile	Ile	Gly	Glu	Tyr	Ala	Gly	Glu	Val	165
				155					160						
Leu	Arg	Phe	Val	Gly	Gly	Ile	Gly	Leu	Phe	Phe	Ser	Phe	Thr	Glu	180
				170					175						
Ile	Leu	Gly	Val	Trp	Leu	Thr	Tyr	Arg	Tyr	Arg	Asn	Gln	Lys	Asp	195
				185					190						
Pro	Arg	Ala	Asn	Pro	Ser	Ala	Phe	Leu							
				200											

<210> 37  
 <211> 390  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336  
 <223> unknown base

<400> 37  
 tgattggagc tgtaaaaaan tcttcaggtg ttgtnatttt tttatatgat 50  
 tattctgtaa nttgtattta ttgttcagtt ttntgtatct tgcgcttggt 100  
 tagccntgaa ccaggagcaa cagggtcagn ttntggaggt tggttggaac 150  
 aatacggcaa gtgctcgaaa tgacatccag agaaatntaa actgctgtgg 200  
 gttccgaagt gttaacccaa atgacacctg tntggctagc tgtgttaaaa 250  
 gtgaccactn gtgctcgcca tgtgctccaa tcataggaga atatgctgga 300  
 gaggttttga gatttggttg tggcattggc ctgttnttca gttttacaga 350  
 gatcctgggt gtttggtgta cctacagata caggaaccag 390

<210> 38  
 <211> 566  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 27

<223> unknown base

<400> 38

aatcccaaat tccccaattt ttttggncctt tttagggaaa gatgtgttgt 50  
ggtaaaaagt gttagtataa aaatgataat ttacttgtag tcttttatga 100  
ttacaccaat gtattctaga atagttatgt cttaggaaat tgtgggttaa 150  
tttttgactt ttacaggtaa gtgcaaagga gaagtgggtt catgaaatgt 200  
tctaattgtat aataacattt accttcagcc tcccatcaga atggaacgag 250  
ttttgagtaa tccaggaagt atatctatat gatcttgata ttgttttata 300  
taatttgaag tctaaaagac tgcattttta aacaagttag tattaatgcg 350  
ttggcccacg tagcaaaaag atatttgatt atcttaaaaa ttgttaaata 400  
ccgttttcat gaaagttctc agtattgtaa cagcaacttg tcaaacctaa 450  
gcatatttga atatgatctc ccataatttg aaattgaaat cgtatttgtgt 500  
ggaggaaatg gcaatcttat gtgtgctgaa ggacacagta agagcaccaa 550  
gttgtgcccc acttgc 566

<210> 39

<211> 264

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 84-85, 206

<223> unknown base

<400> 39

atgattattc tgttacttgt atttattggt cagttttatg gtatcttgcg 50  
cttgttttagc ccctgaaacc aggagcaaca gggnnacgct tcctggaggt 100  
tggttggtcaa caatcacggc caagtgactc cgcaaagac atcccagaga 150  
aatcctaaac tgctgtgggt tccgaagtgt taaccctaat gacacctgtc 200  
tggtctngctg tgtaaaaagt gaccactcgt gctcgccatg tgctccaatc 250  
ataggagaat atgc 264

<210> 40

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 40  
accacgtct gcgttgctgc c 21

<210> 41  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 41  
gagaatatgc tggagagg 18

<210> 42  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 42  
aggaatgcac taggattcgc gcgg 24

<210> 43  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 43  
ggcccaaaag gcaaggacaa agcagctgtc agggaacctc cgccg 45

<210> 44  
<211> 2061  
<212> DNA  
<213> Homo sapiens

<400> 44  
cagtcacat gaagctgggc tgtgtcctca tggcctgggc cctctacctt 50  
tcccttggtg tgctctgggt ggcccagatg ctactggctg ccagttttga 100  
gacgctgcag tgtgaggac ctgtctgcac tgaggagagc agctgccaca 150  
cggaggatga cttgactgat gcaagggaag ctggcttcca ggtcaaggcc 200  
tacactttca gtgaaccctt ccacctgatt gtgtcctatg actggctgat 250  
cctccaaggt ccagccaagc cagtttttga aggggacctg ctggttctgc 300  
gctgccaggc ctggcaagac tggccactga ctcagggtgac cttctaccga 350

gatggctcag ctctgggtcc ccccgggcct aacagggaaat tctccatcac 400  
cgtggtacaa aaggcagaca gcgggcacta ccactgcagt ggcattcttc 450  
agagccctgg tcctgggatc ccagaaacag catctgttgt ggctatcaca 500  
gtccaagaac tgtttccagc gccaatctc agagctgtac cctcagctga 550  
acccaagca ggaagcccca tgacctgag ttgtcagaca aagttgcccc 600  
tgcagaggtc agctgccccg ctcctcttct cttctacaa ggatggaagg 650  
atagtcaaaa gcagggggct ctcctcagaa ttccagatcc ccacagcttc 700  
agaagatcac tccgggtcat actggtgtga ggcagccact gaggacaacc 750  
aagtttgga acagagcccc cagctagaga tcagagtga gggtgcttc 800  
agctctgctg cacctccac attgaatcca gctctcaga aatcagctgc 850  
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cctcatctgt atcaccagat gggccttctt ctcaaacaca tgcaggatgt 1000  
gagagtcctc ctcggtcacc tgctcatgga gttgaggga ttatctggc 1050  
accagaagcc tgggaccaca aaggctactg ctgaatagaa gtaaacagtt 1100  
catccatgat ctacttaac caccocaata aatctgattc tttattttct 1150  
cttctgtcc tgcacatatg cataagtact tttacaagtt gtcccagtg 1200  
tttgtagaa taatgtagt aggtgagtg aaataaattt atataaagt 1250  
agaattagag tttagctata attgtgtatt ctctcttaac acaacagaat 1300  
tctgctgtct agatcaggaa tttctatctg ttatctgac cagaatgttg 1350  
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ggggcaattt tgccccccag aggacattgg gcaatgttg gagacattt 1450  
ggtcattata cttggggggg tgggggatgg tgggatgtgt gtctactggc 1500  
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ggcagtaccc cacaacgaaa aataatctgg cccaaaatgt cagttgtact 1600  
gagtttgaga aaccccagcc taatgaaacc ctaggtgttg ggctctggaa 1650  
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tctagtttgt atccctcaa aagccattat gttgaaatcc taatcccaa 1800

ggtgatggca ttaagaagtg ggcctttggg aagtgattag atcaggagtg 1850  
 cagagccctc atgattagga ttagtgcctt tatttaaaaa ggccccagag 1900  
 agctaactca cccttcacc atatgaggac gtggcaagaa gatgacatgt 1950  
 atgagaacca aaaaacagct gtcgccaac accgactctg tcgttgcctt 2000  
 gatcttgaac ttccagcctc cagaactatg agaaataaaa ttctggttgt 2050  
 ttgtagccta a 2061

<210> 45  
 <211> 359  
 <212> PRT  
 <213> Homo sapiens

<400> 45  
 Met Lys Leu Gly Cys Val Leu Met Ala Trp Ala Leu Tyr Leu Ser  
 1 5 10 15  
 Leu Gly Val Leu Trp Val Ala Gln Met Leu Leu Ala Ala Ser Phe  
 20 25 30  
 Glu Thr Leu Gln Cys Glu Gly Pro Val Cys Thr Glu Glu Ser Ser  
 35 40 45  
 Cys His Thr Glu Asp Asp Leu Thr Asp Ala Arg Glu Ala Gly Phe  
 50 55 60  
 Gln Val Lys Ala Tyr Thr Phe Ser Glu Pro Phe His Leu Ile Val  
 65 70 75  
 Ser Tyr Asp Trp Leu Ile Leu Gln Gly Pro Ala Lys Pro Val Phe  
 80 85 90  
 Glu Gly Asp Leu Leu Val Leu Arg Cys Gln Ala Trp Gln Asp Trp  
 95 100 105  
 Pro Leu Thr Gln Val Thr Phe Tyr Arg Asp Gly Ser Ala Leu Gly  
 110 115 120  
 Pro Pro Gly Pro Asn Arg Glu Phe Ser Ile Thr Val Val Gln Lys  
 125 130 135  
 Ala Asp Ser Gly His Tyr His Cys Ser Gly Ile Phe Gln Ser Pro  
 140 145 150  
 Gly Pro Gly Ile Pro Glu Thr Ala Ser Val Val Ala Ile Thr Val  
 155 160 165  
 Gln Glu Leu Phe Pro Ala Pro Ile Leu Arg Ala Val Pro Ser Ala  
 170 175 180  
 Glu Pro Gln Ala Gly Ser Pro Met Thr Leu Ser Cys Gln Thr Lys  
 185 190 195

Leu	Pro	Leu	Gln	Arg	Ser	Ala	Ala	Arg	Leu	Leu	Phe	Ser	Phe	Tyr	
				200					205					210	
Lys	Asp	Gly	Arg	Ile	Val	Gln	Ser	Arg	Gly	Leu	Ser	Ser	Glu	Phe	
				215					220					225	
Gln	Ile	Pro	Thr	Ala	Ser	Glu	Asp	His	Ser	Gly	Ser	Tyr	Trp	Cys	
				230					235					240	
Glu	Ala	Ala	Thr	Glu	Asp	Asn	Gln	Val	Trp	Lys	Gln	Ser	Pro	Gln	
				245					250					255	
Leu	Glu	Ile	Arg	Val	Gln	Gly	Ala	Ser	Ser	Ser	Ala	Ala	Pro	Pro	
				260					265					270	
Thr	Leu	Asn	Pro	Ala	Pro	Gln	Lys	Ser	Ala	Ala	Pro	Gly	Thr	Ala	
				275					280					285	
Pro	Glu	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Pro	Pro	Pro	Thr	Pro	Ser	
				290					295					300	
Ser	Glu	Asp	Pro	Gly	Phe	Ser	Ser	Pro	Leu	Gly	Met	Pro	Asp	Pro	
				305					310					315	
His	Leu	Tyr	His	Gln	Met	Gly	Leu	Leu	Leu	Lys	His	Met	Gln	Asp	
				320					325					330	
Val	Arg	Val	Leu	Leu	Gly	His	Leu	Leu	Met	Glu	Leu	Arg	Glu	Leu	
				335					340					345	
Ser	Gly	His	Gln	Lys	Pro	Gly	Thr	Thr	Lys	Ala	Thr	Ala	Glu		
				350					355						

<210> 46  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 46  
 tgggctgtgt cctcatgg 18

<210> 47  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 47  
 tttccagcgc caattctc 18

<210> 48



<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 48  
agttcttgga ctgtgatagc cac 23

<210> 49  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 49  
aaacttggtt gtcctcagtg gctg 24

<210> 50  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 50  
gtgagggacc tgtctgcact gaggagagca gctgccacac ggagg 45

<210> 51  
<211> 2181  
<212> DNA  
<213> Homo sapiens

<400> 51  
cccacgcgtc cgcccacgcg tccgcccacg ggtccgccc cgcgtccggg 50  
ccaccagaag tttagcctc tttagtagca ggaggctgga agaaaggaca 100  
gaagtagctc tggctgtgat ggggatctta ctgggcctgc tactcctggg 150  
gcacctaaca gtggacactt atggccgtcc catcctggaa gtgccagaga 200  
gtgtaacagg accttggaag ggggatgtga atcttcctg cacctatgac 250  
cccctgcaag gctacacca agtcttggtg aagtggctgg tacaacgtgg 300  
ctcagaccct gtcaccatct ttctacgtga ctcttctgga gaccatatcc 350  
agcaggcaaa gtaccagggc cgctgcatg tgagccacaa ggttccagga 400  
gatgtatccc tccaattgag caccctggag atggatgacc ggagccacta 450  
cacgtgtgaa gtcacctggc agactcctga tggcaaccaa gtcgtgagag 500

ataagattac tgagctccgt gtccagaaac tctctgtctc caagcccaca 550  
gtgacaactg gcagcgggta tggcttcacg gtgccccagg gaatgaggat 600  
tagccttcaa tgccaggctc ggggttctcc tcccatcagt tatatttggt 650  
ataagcaaca gactaataac caggaacca tcaaagtagc aaccctaagt 700  
accttactct tcaagcctgc ggtgatagcc gactcaggct cctatttctg 750  
cactgccaag ggccagggtg gctctgagca gcacagcgac attgtgaagt 800  
ttgtggtcaa agactcctca aagctactca agaccaagac tgaggcacct 850  
acaaccatga catacccctt gaaagcaaca tctacagtga agcagtcctg 900  
ggactggacc actgacatgg atggctacct tggagagacc agtgctgggc 950  
caggaaagag cctgcctgtc tttgccatca tcctcatcat ctcttgtgc 1000  
tgtatggtgg tttttaccat ggcctatata atgctctgtc ggaagacata 1050  
ccaacaagag catgtctacg aagcagccag gtaagaaagt ctctctctt 1100  
ccatttttga ccccgctcct gccctcaatt ttgattactg gcaggaaatg 1150  
tggaggaagg ggggtgtggc acagacccaa tcctaaggcc ggaggccttc 1200  
agggtcagga catagctgcc ttccctctct caggcacctt ctgaggttgt 1250  
tttgccctc tgaacacaaa ggataattta gatccatctg ccttctgctt 1300  
ccagaatccc tgggtggtag gatcctgata attaattggc aagaattgag 1350  
gcagaagggg gggaaaccag gaccacagcc ccaagtccct tcttatgggt 1400  
ggtgggctct tgggcatag ggcacatgcc agagaggcca acgactctgg 1450  
agaaaccatg aggggtggcca tcttcgcaag tggctgctcc agtgatgagc 1500  
caacttccca gaatctgggc aacaactact ctgatgagcc ctgcatagga 1550  
caggagtacc agatcatcgc ccagatcaat ggcaactacg cccgcctgct 1600  
ggacacagtt cctctggatt atgagtttct ggccactgag ggcaaaagt 1650  
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tcagtccttg ccttctgcat ggccttcttc cctgctacct ctcttctgg 1750  
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ctttgccctg gaatttgcca gatgcctc aagtaagcca gctgctggat 1850  
ttggctctgg gcccttctag tatctctgcc gggggcttct ggtactctc 1900

tctaaatacc agaggaaga tgccatagc actaggactt ggtcatcatg 1950  
 cctacagaca ctattcaact ttggcatctt gccaccagaa gacccgaggg 2000  
 aggctcagct ctgccagctc agaggaccag ctatatccag gatcatttct 2050  
 ctttcttcag ggccagacag cttttaattg aaattgttat ttcacaggcc 2100  
 agggttcagt tctgctctc cactataagt ctaatgttct gactctctcc 2150  
 tgggtctcaa taaatatcta atcataacag c 2181

<210> 52  
 <211> 321  
 <212> PRT  
 <213> Homo sapiens

<400> 52  
 Met Gly Ile Leu Leu Gly Leu Leu Leu Leu Gly His Leu Thr Val  
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 Asp Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr  
                   20                  25                  30  
 Gly Pro Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro  
                   35                  40                  45  
 Leu Gln Gly Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg  
                   50                  55                  60  
 Gly Ser Asp Pro Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp  
                   65                  70                  75  
 His Ile Gln Gln Ala Lys Tyr Gln Gly Arg Leu His Val Ser His  
                   80                  85                  90  
 Lys Val Pro Gly Asp Val Ser Leu Gln Leu Ser Thr Leu Glu Met  
                   95                  100                  105  
 Asp Asp Arg Ser His Tyr Thr Cys Glu Val Thr Trp Gln Thr Pro  
                   110                  115                  120  
 Asp Gly Asn Gln Val Val Arg Asp Lys Ile Thr Glu Leu Arg Val  
                   125                  130                  135  
 Gln Lys Leu Ser Val Ser Lys Pro Thr Val Thr Thr Gly Ser Gly  
                   140                  145                  150  
 Tyr Gly Phe Thr Val Pro Gln Gly Met Arg Ile Ser Leu Gln Cys  
                   155                  160                  165  
 Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile Trp Tyr Lys Gln  
                   170                  175                  180  
 Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr Leu Ser Thr  
                   185                  190                  195

Leu	Leu	Phe	Lys	Pro	Ala	Val	Ile	Ala	Asp	Ser	Gly	Ser	Tyr	Phe	
				200					205					210	
Cys	Thr	Ala	Lys	Gly	Gln	Val	Gly	Ser	Glu	Gln	His	Ser	Asp	Ile	
				215					220					225	
Val	Lys	Phe	Val	Val	Lys	Asp	Ser	Ser	Lys	Leu	Leu	Lys	Thr	Lys	
				230					235					240	
Thr	Glu	Ala	Pro	Thr	Thr	Met	Thr	Tyr	Pro	Leu	Lys	Ala	Thr	Ser	
				245					250					255	
Thr	Val	Lys	Gln	Ser	Trp	Asp	Trp	Thr	Thr	Asp	Met	Asp	Gly	Tyr	
				260					265					270	
Leu	Gly	Glu	Thr	Ser	Ala	Gly	Pro	Gly	Lys	Ser	Leu	Pro	Val	Phe	
				275					280					285	
Ala	Ile	Ile	Leu	Ile	Ile	Ser	Leu	Cys	Cys	Met	Val	Val	Phe	Thr	
				290					295					300	
Met	Ala	Tyr	Ile	Met	Leu	Cys	Arg	Lys	Thr	Ser	Gln	Gln	Glu	His	
				305					310					315	
Val	Tyr	Glu	Ala	Ala	Arg										
				320											

<210> 53  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 53  
 tatccctcca attgagcacc ctgg 24

<210> 54  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 54  
 gtcggaagac atcccaacaa g 21

<210> 55  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 55  
cttcacaatg tcgctgtgct gctc 24

<210> 56  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 56  
agccaaatcc agcagctggc ttac 24

<210> 57  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 57  
tggatgaccg gagccactac acgtgtgaag tcacctggca gactcctgat 50

<210> 58  
<211> 2458  
<212> DNA  
<213> Homo sapiens

<400> 58  
gcgccgggag cccatctgcc ccagggggca cggggcgcg ggccggctcc 50  
cgccccggcac atggctgcag ccacctcgcg cgcaccccga ggccggcgcg 100  
ccagctcgcc cgaggtccgt cggaggcgcc cggccgcccc ggagccaagc 150  
agcaactgag cggggaagcg cccgcgtccg gggatcgga tgtccctcct 200  
ccttctcctc ttgctagttt cctactatgt tggaaccttg gggactcaca 250  
ctgagatcaa gagagtggca gaggaaaagg tcactttgcc ctgccaccat 300  
caactggggc ttccagaaaa agacactctg gatattgaat ggctgctcac 350  
cgataatgaa gggaaccaaa aagtgggtgat cacttactcc agtcgtcatg 400  
tctacaataa cttgactgag gaacagaagg gccgagtggc ctttgcttcc 450  
aatttcctgg caggagatgc ctccttgagc attgaacctc tgaagcccag 500  
tgatgagggc cggtagacct gtaagggtta gaattcaggg cgctacgtgt 550  
ggagccatgt catcttaaaa gtcttagtga gaccatccaa gcccaagtgt 600  
gagttggaag gagagctgac agaaggaagt gacctgactt tgcagtgtga 650

gtcatcctct ggcacagagc ccattgtgta ttactggcag cgaatccgag 700  
agaaagaggg agaggatgaa cgtctgcctc ccaaactag gattgactac 750  
aaccaccctg gacgagttct gctgcagaat cttaccatgt cctactctgg 800  
actgtaccag tgcacagcag gcaacgaagc tgggaaggaa agctgtgtgg 850  
tgcgagtaac tgtacagtat gtacaaagca tcggcatggt tgcaggagca 900  
gtgacaggca tagtggctgg agccctgctg attttctct tgggtgtggct 950  
gctaatccga aggaaagaca aagaaagata tgaggaagaa gagagaccta 1000  
atgaaattcg agaagatgct gaagctccaa aagcccgtct tgtgaaaccc 1050  
agctcctctt cctcaggctc tcggagctca cgctctgggt cttcctccac 1100  
tcgctccaca gcaaatagtg cctcacgcag ccagcggaca ctgtcaactg 1150  
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 <211> 373  
 <212> PRT  
 <213> Homo sapiens

<400> 59  
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 Thr Leu Asp Ile Glu Trp Leu Leu Thr Asp Asn Glu Gly Asn Gln  
 50 55 60  
 Lys Val Val Ile Thr Tyr Ser Ser Arg His Val Tyr Asn Asn Leu  
 65 70 75  
 Thr Glu Glu Gln Lys Gly Arg Val Ala Phe Ala Ser Asn Phe Leu  
 80 85 90  
 Ala Gly Asp Ala Ser Leu Gln Ile Glu Pro Leu Lys Pro Ser Asp  
 95 100 105  
 Glu Gly Arg Tyr Thr Cys Lys Val Lys Asn Ser Gly Arg Tyr Val  
 110 115 120  
 Trp Ser His Val Ile Leu Lys Val Leu Val Arg Pro Ser Lys Pro  
 125 130 135  
 Lys Cys Glu Leu Glu Gly Glu Leu Thr Glu Gly Ser Asp Leu Thr  
 140 145 150  
 Leu Gln Cys Glu Ser Ser Ser Gly Thr Glu Pro Ile Val Tyr Tyr  
 155 160 165  
 Trp Gln Arg Ile Arg Glu Lys Glu Gly Glu Asp Glu Arg Leu Pro

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Pro Lys Ser Arg Ile Asp Tyr Asn His	Pro Gly Arg Val Leu Leu	
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Gln Asn Leu Thr Met Ser Tyr Ser Gly	Leu Tyr Gln Cys Thr	Ala
200	205	210
Gly Asn Glu Ala Gly Lys Glu Ser Cys	Val Val Arg Val Thr	Val
215	220	225
Gln Tyr Val Gln Ser Ile Gly Met Val	Ala Gly Ala Val Thr	Gly
230	235	240
Ile Val Ala Gly Ala Leu Leu Ile Phe	Leu Leu Val Trp Leu Leu	
245	250	255
Ile Arg Arg Lys Asp Lys Glu Arg Tyr	Glu Glu Glu Glu Arg	Pro
260	265	270
Asn Glu Ile Arg Glu Asp Ala Glu Ala	Pro Lys Ala Arg Leu Val	
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Lys Pro Ser Ser Ser Ser Ser Gly Ser	Arg Ser Ser Arg Ser	Gly
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Ser Ser Ser Thr Arg Ser Thr Ala Asn	Ser Ala Ser Arg Ser	Gln
305	310	315
Arg Thr Leu Ser Thr Asp Ala Ala Pro	Gln Pro Gly Leu Ala Thr	
320	325	330
Gln Ala Tyr Ser Leu Val Gly Pro Glu	Val Arg Gly Ser Glu	Pro
335	340	345
Lys Lys Val His His Ala Asn Leu Thr	Lys Ala Glu Thr Thr	Pro
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 60

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<210> 61

<211> 24

<212> DNA

<213> Artificial Sequence



<220>

<223> Synthetic oligonucleotide probe

<400> 61

actaggctgt atgcctgggt gggc 24

<210> 62

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 62

gtatgtacaa agcatcggca tggttgcagg agcagtgaca ggc 43

<210> 63

<211> 3534

<212> DNA

<213> Homo sapiens

<400> 63

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<210> 64

<211> 655

<212> PRT

<213> Homo sapiens

<400> 64

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Arg	Ile	Ala	Arg	Arg	Ala	Thr	Ala	Thr	Met	Ile	Ala	Gly	Ser	Leu		20	25		30
Leu	Leu	Leu	Gly	Phe	Leu	Ser	Thr	Thr	Thr	Ala	Gln	Pro	Glu	Gln		35	40		45
Lys	Ala	Ser	Asn	Leu	Ile	Gly	Thr	Tyr	Arg	His	Val	Asp	Arg	Ala		50	55		60
Thr	Gly	Gln	Val	Leu	Thr	Cys	Asp	Lys	Cys	Pro	Ala	Gly	Thr	Tyr		65	70		75
Val	Ser	Glu	His	Cys	Thr	Asn	Thr	Ser	Leu	Arg	Val	Cys	Ser	Ser		80	85		90
Cys	Pro	Val	Gly	Thr	Phe	Thr	Arg	His	Glu	Asn	Gly	Ile	Glu	Lys		95	100		105
Cys	His	Asp	Cys	Ser	Gln	Pro	Cys	Pro	Trp	Pro	Met	Ile	Glu	Lys		110	115		120
Leu	Pro	Cys	Ala	Ala	Leu	Thr	Asp	Arg	Glu	Cys	Thr	Cys	Pro	Pro		125	130		135
Gly	Met	Phe	Gln	Ser	Asn	Ala	Thr	Cys	Ala	Pro	His	Thr	Val	Cys		140	145		150
Pro	Val	Gly	Trp	Gly	Val	Arg	Lys	Lys	Gly	Thr	Glu	Thr	Glu	Asp		155	160		165
Val	Arg	Cys	Lys	Gln	Cys	Ala	Arg	Gly	Thr	Phe	Ser	Asp	Val	Pro		170	175		180
Ser	Ser	Val	Met	Lys	Cys	Lys	Ala	Tyr	Thr	Asp	Cys	Leu	Ser	Gln		185	190		195
Asn	Leu	Val	Val	Ile	Lys	Pro	Gly	Thr	Lys	Glu	Thr	Asp	Asn	Val		200	205		210
Cys	Gly	Thr	Leu	Pro	Ser	Phe	Ser	Ser	Ser	Thr	Ser	Pro	Ser	Pro		215	220		225
Gly	Thr	Ala	Ile	Phe	Pro	Arg	Pro	Glu	His	Met	Glu	Thr	His	Glu		230	235		240
Val	Pro	Ser	Ser	Thr	Tyr	Val	Pro	Lys	Gly	Met	Asn	Ser	Thr	Glu		245	250		255
Ser	Asn	Ser	Ser	Ala	Ser	Val	Arg	Pro	Lys	Val	Leu	Ser	Ser	Ile		260	265		270
Gln	Glu	Gly	Thr	Val	Pro	Asp	Asn	Thr	Ser	Ser	Ala	Arg	Gly	Lys		275	280		285

Glu Asp Val Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His	290	295	300
Gln Gln Gly Pro His His Arg His Ile Leu Lys Leu Leu Pro Ser	305	310	315
Met Glu Ala Thr Gly Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly	320	325	330
Pro Lys Arg Gly His Pro Arg Gln Asn Leu His Lys His Phe Asp	335	340	345
Ile Asn Glu His Leu Pro Trp Met Ile Val Leu Phe Leu Leu Leu	350	355	360
Val Leu Val Val Ile Val Val Cys Ser Ile Arg Lys Ser Ser Arg	365	370	375
Thr Leu Lys Lys Gly Pro Arg Gln Asp Pro Ser Ala Ile Val Glu	380	385	390
Lys Ala Gly Leu Lys Lys Ser Met Thr Pro Thr Gln Asn Arg Glu	395	400	405
Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Ile Asp Ile Leu Lys	410	415	420
Leu Val Ala Ala Gln Val Gly Ser Gln Trp Lys Asp Ile Tyr Gln	425	430	435
Phe Leu Cys Asn Ala Ser Glu Arg Glu Val Ala Ala Phe Ser Asn	440	445	450
Gly Tyr Thr Ala Asp His Glu Arg Ala Tyr Ala Ala Leu Gln His	455	460	465
Trp Thr Ile Arg Gly Pro Glu Ala Ser Leu Ala Gln Leu Ile Ser	470	475	480
Ala Leu Arg Gln His Arg Arg Asn Asp Val Val Glu Lys Ile Arg	485	490	495
Gly Leu Met Glu Asp Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala	500	505	510
Leu Pro Met Ser Pro Ser Pro Leu Ser Pro Ser Pro Ile Pro Ser	515	520	525
Pro Asn Ala Lys Leu Glu Asn Ser Ala Leu Leu Thr Val Glu Pro	530	535	540
Ser Pro Gln Asp Lys Asn Lys Gly Phe Phe Val Asp Glu Ser Glu	545	550	555
Pro Leu Leu Arg Cys Asp Ser Thr Ser Ser Gly Ser Ser Ala Leu	560	565	570

Ser	Arg	Asn	Gly	Ser	Phe	Ile	Thr	Lys	Glu	Lys	Lys	Asp	Thr	Val	
				575					580					585	
Leu	Arg	Gln	Val	Arg	Leu	Asp	Pro	Cys	Asp	Leu	Gln	Pro	Ile	Phe	
				590					595					600	
Asp	Asp	Met	Leu	His	Phe	Leu	Asn	Pro	Glu	Glu	Leu	Arg	Val	Ile	
				605					610					615	
Glu	Glu	Ile	Pro	Gln	Ala	Glu	Asp	Lys	Leu	Asp	Arg	Leu	Phe	Glu	
				620					625					630	
Ile	Ile	Gly	Val	Lys	Ser	Gln	Glu	Ala	Ser	Gln	Thr	Leu	Leu	Asp	
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Ser	Val	Tyr	Ser	His	Leu	Pro	Asp	Leu	Leu						
				650					655						

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 65

gtagcagtgc acatggggtg ttgg 24

<210> 66

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 66

accgcacatc ctcaagtctct gtcc 24

<210> 67

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 67

acgatgatcg cgggctccct tctcctgctt ggattcctta gcaccaccac 50

<210> 68

<211> 2412

<212> DNA

<213> Homo sapiens

<400> 68

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<210> 69

<211> 453

<212> PRT

<213> Homo sapiens

<400> 69

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				20					25					30

Pro	Asp	Ala	Asp	Ala	Val	Ala	Ala	Gln	Ile	Leu	Ser	Leu	Leu	Pro
				35					40					45

Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile



[illegible]

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	350	355	360		
Val Pro Leu Ile	Ser Asn Lys Ile Cys	Asn His Arg Asp	Val Tyr		
	365	370	375		
Gly Gly Ile Ile	Ser Pro Ser Met Leu	Cys Ala Gly Tyr	Leu Thr		
	380	385	390		
Gly Gly Val Asp	Ser Cys Gln Gly Asp	Ser Gly Gly Pro	Leu Val		
	395	400	405		
Cys Gln Glu Arg	Arg Leu Trp Lys Leu	Val Gly Ala Thr	Ser Phe		
	410	415	420		
Gly Ile Gly Cys	Ala Glu Val Asn Lys	Pro Gly Val Tyr	Thr Arg		
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Leu Lys Thr

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<400> 72

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<210> 73

<211> 3305

<212> DNA

<213> Homo sapiens

<400> 73

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<210> 74

<211> 735

<212> PRT

<213> Homo sapiens

<400> 74

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Val	Ser	Leu	Trp	Asn	Gln	Gly	Arg	Ala	Asp	Glu	Val	Val	Ser	Ala	35	40	45	
Ser	Val	Arg	Ser	Gly	Asp	Leu	Trp	Ile	Pro	Val	Lys	Ser	Phe	Asp	50	55	60	
Ser	Lys	Asn	His	Pro	Glu	Val	Leu	Asn	Ile	Arg	Leu	Gln	Arg	Glu	65	70	75	
Ser	Lys	Glu	Leu	Ile	Ile	Asn	Leu	Glu	Arg	Asn	Glu	Gly	Leu	Ile	80	85	90	
Ala	Ser	Ser	Phe	Thr	Glu	Thr	His	Tyr	Leu	Gln	Asp	Gly	Thr	Asp	95	100	105	
Val	Ser	Leu	Ala	Arg	Asn	Tyr	Thr	Gly	His	Cys	Tyr	Tyr	His	Gly	110	115	120	

His Val Arg Gly Tyr Ser Asp Ser Ala Val Ser Leu Ser Thr Cys	125	130	135
Ser Gly Leu Arg Gly Leu Ile Val Phe Glu Asn Glu Ser Tyr Val	140	145	150
Leu Glu Pro Met Lys Ser Ala Thr Asn Arg Tyr Lys Leu Phe Pro	155	160	165
Ala Lys Lys Leu Lys Ser Val Arg Gly Ser Cys Gly Ser His His	170	175	180
Asn Thr Pro Asn Leu Ala Ala Lys Asn Val Phe Pro Pro Pro Ser	185	190	195
Gln Thr Trp Ala Arg Arg His Lys Arg Glu Thr Leu Lys Ala Thr	200	205	210
Lys Tyr Val Glu Leu Val Ile Val Ala Asp Asn Arg Glu Phe Gln	215	220	225
Arg Gln Gly Lys Asp Leu Glu Lys Val Lys Gln Arg Leu Ile Glu	230	235	240
Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro Leu Asn Ile Arg	245	250	255
Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met Asp Lys Cys	260	265	270
Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe Leu Asp	275	280	285
Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn Ala	290	295	300
Gln Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met	305	310	315
Ala Pro Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly Ile	320	325	330
Val Met Asp His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr Leu	335	340	345
Ala His Glu Leu Gly His Asn Phe Gly Met Asn His Asp Thr Leu	350	355	360
Asp Arg Gly Cys Ser Cys Gln Met Ala Val Glu Lys Gly Gly Cys	365	370	375
Ile Met Asn Ala Ser Thr Gly Tyr Pro Phe Pro Met Val Phe Ser	380	385	390
Ser Cys Ser Arg Lys Asp Leu Glu Thr Ser Leu Glu Lys Gly Met	395	400	405

Gly Val Cys Leu Phe Asn Leu Pro Glu	Val Arg Glu Ser Phe Gly	410	415	420
Gly Gln Lys Cys Gly Asn Arg Phe Val	Glu Glu Gly Glu Glu Cys	425	430	435
Asp Cys Gly Glu Pro Glu Glu Cys Met	Asn Arg Cys Cys Asn Ala	440	445	450
Thr Thr Cys Thr Leu Lys Pro Asp Ala	Val Cys Ala His Gly Leu	455	460	465
Cys Cys Glu Asp Cys Gln Leu Lys Pro	Ala Gly Thr Ala Cys Arg	470	475	480
Asp Ser Ser Asn Ser Cys Asp Leu Pro	Glu Phe Cys Thr Gly Ala	485	490	495
Ser Pro His Cys Pro Ala Asn Val Tyr	Leu His Asp Gly His Ser	500	505	510
Cys Gln Asp Val Asp Gly Tyr Cys Tyr	Asn Gly Ile Cys Gln Thr	515	520	525
His Glu Gln Gln Cys Val Thr Leu Trp	Gly Pro Gly Ala Lys Pro	530	535	540
Ala Pro Gly Ile Cys Phe Glu Arg Val	Asn Ser Ala Gly Asp Pro	545	550	555
Tyr Gly Asn Cys Gly Lys Val Ser Lys	Ser Ser Phe Ala Lys Cys	560	565	570
Glu Met Arg Asp Ala Lys Cys Gly Lys	Ile Gln Cys Gln Gly Gly	575	580	585
Ala Ser Arg Pro Val Ile Gly Thr Asn	Ala Val Ser Ile Glu Thr	590	595	600
Asn Ile Pro Leu Gln Gln Gly Gly Arg	Ile Leu Cys Arg Gly Thr	605	610	615
His Val Tyr Leu Gly Asp Asp Met Pro	Asp Pro Gly Leu Val Leu	620	625	630
Ala Gly Thr Lys Cys Ala Asp Gly Lys	Ile Cys Leu Asn Arg Gln	635	640	645
Cys Gln Asn Ile Ser Val Phe Gly Val	His Glu Cys Ala Met Gln	650	655	660
Cys His Gly Arg Gly Val Cys Asn Asn	Arg Lys Asn Cys His Cys	665	670	675
Glu Ala His Trp Ala Pro Pro Phe Cys	Asp Lys Phe Gly Phe Gly	680	685	690

Gly Ser Thr Asp Ser Gly Pro Ile Arg Gln Ala Glu Ala Arg Gln  
695 700 705

Glu Ala Ala Glu Ser Asn Arg Glu Arg Gly Gln Gly Gln Glu Pro  
710 715 720

Val Gly Ser Gln Glu His Ala Ser Thr Ala Ser Leu Thr Leu Ile  
725 730 735

<210> 75

<211> 483

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 94, 143, 156, 163, 179, 193, 369, 371, 381, 390, 473

<223> unknown base

<400> 75

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gcagccctga taactggtnt ntggctgcaa nttaatgctn tgatatggct 400  
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<220>

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<400> 76

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<210> 77

<211> 18

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<213> Artificial Sequence



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<223> Synthetic oligonucleotide probe

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<210> 85

<211> 67

<212> PRT

<213> Homo sapiens

<400> 85

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Leu	Ala	Leu	Leu	Leu	Pro	Val	Gln	Val	Ser	Ser	Phe	Val	Pro	Leu
				20				25					30	

Thr	Ser	Met	Pro	Glu	Ala	Thr	Ala	Ala	Glu	Thr	Thr	Lys	Pro	Ser
				35				40					45	

Asn	Ser	Ala	Leu	Gln	Pro	Thr	Ala	Gly	Leu	Leu	Val	Val	Leu	Leu
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Ala	Leu	Leu	His	Leu	Tyr	His
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<400> 87  
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<212> DNA  
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<210> 90

<211> 432

<212> PRT

<213> Homo sapiens

<400> 90

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				20					25					30

Gly	Gly	Arg	Trp	Gly	Ala	Arg	Ala	Gln	Glu	Ala	Ala	Ala	Ala	Ala
				35					40					45

Ala Asp Gly Pro Pro Ala Ala Asp Gly Glu Asp Gly Gln Asp Pro	50	55	60
His Ser Lys His Leu Tyr Thr Ala Asp Met Phe Thr His Gly Ile	65	70	75
Gln Ser Ala Ala His Phe Val Met Phe Phe Ala Pro Trp Cys Gly	80	85	90
His Cys Gln Arg Leu Gln Pro Thr Trp Asn Asp Leu Gly Asp Lys	95	100	105
Tyr Asn Ser Met Glu Asp Ala Lys Val Tyr Val Ala Lys Val Asp	110	115	120
Cys Thr Ala His Ser Asp Val Cys Ser Ala Gln Gly Val Arg Gly	125	130	135
Tyr Pro Thr Leu Lys Leu Phe Lys Pro Gly Gln Glu Ala Val Lys	140	145	150
Tyr Gln Gly Pro Arg Asp Phe Gln Thr Leu Glu Asn Trp Met Leu	155	160	165
Gln Thr Leu Asn Glu Glu Pro Val Thr Pro Glu Pro Glu Val Glu	170	175	180
Pro Pro Ser Ala Pro Glu Leu Lys Gln Gly Leu Tyr Glu Leu Ser	185	190	195
Ala Ser Asn Phe Glu Leu His Val Ala Gln Gly Asp His Phe Ile	200	205	210
Lys Phe Phe Ala Pro Trp Cys Gly His Cys Lys Ala Leu Ala Pro	215	220	225
Thr Trp Glu Gln Leu Ala Leu Gly Leu Glu His Ser Glu Thr Val	230	235	240
Lys Ile Gly Lys Val Asp Cys Thr Gln His Tyr Glu Leu Cys Ser	245	250	255
Gly Asn Gln Val Arg Gly Tyr Pro Thr Leu Leu Trp Phe Arg Asp	260	265	270
Gly Lys Lys Val Asp Gln Tyr Lys Gly Lys Arg Asp Leu Glu Ser	275	280	285
Leu Arg Glu Tyr Val Glu Ser Gln Leu Gln Arg Thr Glu Thr Gly	290	295	300
Ala Thr Glu Thr Val Thr Pro Ser Glu Ala Pro Val Leu Ala Ala	305	310	315
Glu Pro Glu Ala Asp Lys Gly Thr Val Leu Ala Leu Thr Glu Asn	320	325	330

Asn Phe Asp Asp Thr Ile Ala Glu Gly Ile Thr Phe Ile Lys Phe  
335 340 345

Tyr Ala Pro Trp Cys Gly His Cys Lys Thr Leu Ala Pro Thr Trp  
350 355 360

Glu Glu Leu Ser Lys Lys Glu Phe Pro Gly Leu Ala Gly Val Lys  
365 370 375

Ile Ala Glu Val Asp Cys Thr Ala Glu Arg Asn Ile Cys Ser Lys  
380 385 390

Tyr Ser Val Arg Gly Tyr Pro Thr Leu Leu Leu Phe Arg Gly Gly  
395 400 405

Lys Lys Val Ser Glu His Ser Gly Gly Arg Asp Leu Asp Ser Leu  
410 415 420

His Arg Phe Val Leu Ser Gln Ala Lys Asp Glu Leu  
425 430

<210> 91

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 91

atgttcttcg cgccctggtg 20

<210> 92

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 92

ccaagccaac acactctaca g 21

<210> 93

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 93

aagtggtcgc cttgtgcaac gtgc 24

<210> 94

<211> 23



<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 94  
ggtcaaaggg gatatatcgc cac 23

<210> 95  
<211> 49  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 95  
gcatggaaga tgccaaagtc tatgtggcta aagtggactg cacggccca 49

<210> 96  
<211> 1016  
<212> DNA  
<213> Homo sapiens

<400> 96  
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gtctggatat tgatagccgt cctaccgctg aagtctgtgc cacacacaca 150  
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 agtcaacata gctagaaaaat gctaaaactga ggtatggagc ctccatcatc 1000  
 aaaaaaaaaa aaaaaa 1016

<210> 97  
 <211> 277  
 <212> PRT  
 <213> Homo sapiens

<400> 97  
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 20 25 30  
 Asp Ser Arg Pro Thr Ala Glu Val Cys Ala Thr His Thr Ile Ser  
 35 40 45  
 Pro Gly Pro Lys Gly Asp Asp Gly Glu Lys Gly Asp Pro Gly Glu  
 50 55 60  
 Glu Gly Lys His Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile  
 65 70 75  
 Lys Gly Glu Leu Gly Asp Met Gly Asp Gln Gly Asn Ile Gly Lys  
 80 85 90  
 Thr Gly Pro Ile Gly Lys Lys Gly Asp Lys Gly Glu Lys Gly Leu  
 95 100 105  
 Leu Gly Ile Pro Gly Glu Lys Gly Lys Ala Gly Thr Val Cys Asp  
 110 115 120  
 Cys Gly Arg Tyr Arg Lys Phe Val Gly Gln Leu Asp Ile Ser Ile  
 125 130 135  
 Ala Arg Leu Lys Thr Ser Met Lys Phe Val Lys Asn Val Ile Ala  
 140 145 150  
 Gly Ile Arg Glu Thr Glu Glu Lys Phe Tyr Tyr Ile Val Gln Glu  
 155 160 165  
 Glu Lys Asn Tyr Arg Glu Ser Leu Thr His Cys Arg Ile Arg Gly  
 170 175 180  
 Gly Met Leu Ala Met Pro Lys Asp Glu Ala Ala Asn Thr Leu Ile  
 185 190 195  
 Ala Asp Tyr Val Ala Lys Ser Gly Phe Phe Arg Val Phe Ile Gly

	200	205	210
Val Asn Asp Leu	Glu Arg Glu Gly Gln	Tyr Met Ser Thr Asp	Asn
	215	220	225
Thr Pro Leu Gln	Asn Tyr Ser Asn Trp	Asn Glu Gly Glu Pro	Ser
	230	235	240
Asp Pro Tyr Gly	His Glu Asp Cys Val	Glu Met Leu Ser Ser	Gly
	245	250	255
Arg Trp Asn Asp	Thr Glu Cys His Leu	Thr Met Tyr Phe Val	Cys
	260	265	270
Glu Phe Ile Lys	Lys Lys Lys		
	275		

<210> 98  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 98  
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<210> 99  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 99  
 gatgatggag gctccatacc tcag 24

<210> 100  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 100  
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<210> 101  
 <211> 2574  
 <212> DNA  
 <213> Homo sapiens

<400> 101  
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gggcctgggt gggaatgggc gtgtgccagc gcacgcgcgc tccctggaag 150  
gagaagtctc agctagaacg agcggcccta ggttttcgga agggaggatc 200  
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<210> 102

<211> 730

<212> PRT

<213> Homo sapiens

<400> 102

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Gln	Leu	Glu	Arg	Ala	Ala	Leu	Gly	Phe	Arg	Lys	Gly	Gly	Ser	Gly
				20					25					30

Met	Phe	Ala	Ser	Gly	Trp	Asn	Gln	Thr	Val	Pro	Ile	Glu	Glu	Ala	35	40	45
Gly	Ser	Met	Ala	Ala	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	50	55	60
Pro	Leu	Leu	Leu	Leu	Lys	Leu	His	Leu	Trp	Pro	Gln	Leu	Arg	Trp	65	70	75
Leu	Pro	Ala	Asp	Leu	Ala	Phe	Ala	Val	Arg	Ala	Leu	Cys	Cys	Lys	80	85	90
Arg	Ala	Leu	Arg	Ala	Arg	Ala	Leu	Ala	Ala	Ala	Ala	Ala	Asp	Pro	95	100	105
Glu	Gly	Pro	Glu	Gly	Gly	Cys	Ser	Leu	Ala	Trp	Arg	Leu	Ala	Glu	110	115	120
Leu	Ala	Gln	Gln	Arg	Ala	Ala	His	Thr	Phe	Leu	Ile	His	Gly	Ser	125	130	135
Arg	Arg	Phe	Ser	Tyr	Ser	Glu	Ala	Glu	Arg	Glu	Ser	Asn	Arg	Ala	140	145	150
Ala	Arg	Ala	Phe	Leu	Arg	Ala	Leu	Gly	Trp	Asp	Trp	Gly	Pro	Asp	155	160	165
Gly	Gly	Asp	Ser	Gly	Glu	Gly	Ser	Ala	Gly	Glu	Gly	Glu	Arg	Ala	170	175	180
Ala	Pro	Gly	Ala	Gly	Asp	Ala	Ala	Ala	Gly	Ser	Gly	Ala	Glu	Phe	185	190	195
Ala	Gly	Gly	Asp	Gly	Ala	Ala	Arg	Gly	Gly	Gly	Ala	Ala	Ala	Pro	200	205	210
Leu	Ser	Pro	Gly	Ala	Thr	Val	Ala	Leu	Leu	Leu	Pro	Ala	Gly	Pro	215	220	225
Glu	Phe	Leu	Trp	Leu	Trp	Phe	Gly	Leu	Ala	Lys	Ala	Gly	Leu	Arg	230	235	240
Thr	Ala	Phe	Val	Pro	Thr	Ala	Leu	Arg	Arg	Gly	Pro	Leu	Leu	His	245	250	255
Cys	Leu	Arg	Ser	Cys	Gly	Ala	Arg	Ala	Leu	Val	Leu	Ala	Pro	Glu	260	265	270
Phe	Leu	Glu	Ser	Leu	Glu	Pro	Asp	Leu	Pro	Ala	Leu	Arg	Ala	Met	275	280	285
Gly	Leu	His	Leu	Trp	Ala	Ala	Gly	Pro	Gly	Thr	His	Pro	Ala	Gly	290	295	300
Ile	Ser	Asp	Leu	Leu	Ala	Glu	Val	Ser	Ala	Glu	Val	Asp	Gly	Pro	305	310	315

Val Pro Gly Tyr	Leu Ser Ser Pro Gln Ser Ile Thr Asp Thr Cys	320	325	330
Leu Tyr Ile Phe	Thr Ser Gly Thr Thr Gly Leu Pro Lys Ala Ala	335	340	345
Arg Ile Ser His	Leu Lys Ile Leu Gln Cys Gln Gly Phe Tyr Gln	350	355	360
Leu Cys Gly Val	His Gln Glu Asp Val Ile Tyr Leu Ala Leu Pro	365	370	375
Leu Tyr His Met	Ser Gly Ser Leu Leu Gly Ile Val Gly Cys Met	380	385	390
Gly Ile Gly Ala	Thr Val Val Leu Lys Ser Lys Phe Ser Ala Gly	395	400	405
Gln Phe Trp Glu	Asp Cys Gln Gln His Arg Val Thr Val Phe Gln	410	415	420
Tyr Ile Gly Glu	Leu Cys Arg Tyr Leu Val Asn Gln Pro Pro Ser	425	430	435
Lys Ala Glu Arg	Gly His Lys Val Arg Leu Ala Val Gly Ser Gly	440	445	450
Leu Arg Pro Asp	Thr Trp Glu Arg Phe Val Arg Arg Phe Gly Pro	455	460	465
Leu Gln Val Leu	Glu Thr Tyr Gly Leu Thr Glu Gly Asn Val Ala	470	475	480
Thr Ile Asn Tyr	Thr Gly Gln Arg Gly Ala Val Gly Arg Ala Ser	485	490	495
Trp Leu Tyr Lys	His Ile Phe Pro Phe Ser Leu Ile Arg Tyr Asp	500	505	510
Val Thr Thr Gly	Glu Pro Ile Arg Asp Pro Gln Gly His Cys Met	515	520	525
Ala Thr Ser Pro	Gly Glu Pro Gly Leu Leu Val Ala Pro Val Ser	530	535	540
Gln Gln Ser Pro	Phe Leu Gly Tyr Ala Gly Gly Pro Glu Leu Ala	545	550	555
Gln Gly Lys Leu	Leu Lys Asp Val Phe Arg Pro Gly Asp Val Phe	560	565	570
Phe Asn Thr Gly	Asp Leu Leu Val Cys Asp Asp Gln Gly Phe Leu	575	580	585
Arg Phe His Asp	Arg Thr Gly Asp Thr Phe Arg Trp Lys Gly Glu	590	595	600

Asn Val Ala Thr Thr Glu Val Ala Glu Val Phe Glu Ala Leu Asp		
	605	610 615
Phe Leu Gln Glu Val Asn Val Tyr Gly Val Thr Val Pro Gly His		
	620	625 630
Glu Gly Arg Ala Gly Met Ala Ala Leu Val Leu Arg Pro Pro His		
	635	640 645
Ala Leu Asp Leu Met Gln Leu Tyr Thr His Val Ser Glu Asn Leu		
	650	655 660
Pro Pro Tyr Ala Arg Pro Arg Phe Leu Arg Leu Gln Glu Ser Leu		
	665	670 675
Ala Thr Thr Glu Thr Phe Lys Gln Gln Lys Val Arg Met Ala Asn		
	680	685 690
Glu Gly Phe Asp Pro Ser Thr Leu Ser Asp Pro Leu Tyr Val Leu		
	695	700 705
Asp Gln Ala Val Gly Ala Tyr Leu Pro Leu Thr Thr Ala Arg Tyr		
	710	715 720
Ser Ala Leu Leu Ala Gly Asn Leu Arg Ile		
	725	730

<210> 103  
 <211> 22  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 103  
 gagagccatg gggctccacc tg 22

<210> 104  
 <211> 18  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 104  
 ggagaatgtg gccacaac 18

<210> 105  
 <211> 26  
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<220>  
 <223> Synthetic oligonucleotide probe



<400> 105  
gccctggcac agtgactcca tagacg 26

<210> 106  
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<212> DNA  
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<400> 106  
atccacttca gcggacac 18

<210> 107  
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<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 107  
ccagtgcag gatacctctc ttccccccag agcataacag acacg 45

<210> 108  
<211> 2579  
<212> DNA  
<213> Homo sapiens

<400> 108  
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acgcgcgcat acacactcgc tctcgtttgt ccatctccct cccgggggag 150  
  
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<210> 109

<211> 555

<212> PRT

<213> Homo sapiens

<400> 109

Met	Pro	Ser	Trp	Ile	Gly	Ala	Val	Ile	Leu	Pro	Leu	Leu	Gly	Leu
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Leu	Leu	Ser	Leu	Pro	Ala	Gly	Ala	Asp	Val	Lys	Ala	Arg	Ser	Cys
			20						25					30

Gly	Glu	Val	Arg	Gln	Ala	Tyr	Gly	Ala	Lys	Gly	Phe	Ser	Leu	Ala
				35					40					45

Asp	Ile	Pro	Tyr	Gln	Glu	Ile	Ala	Gly	Glu	His	Leu	Arg	Ile	Cys
				50					55					60

Pro	Gln	Glu	Tyr	Thr	Cys	Cys	Thr	Thr	Glu	Met	Glu	Asp	Lys	Leu
				65					70					75

Ser	Gln	Gln	Ser	Lys	Leu	Glu	Phe	Glu	Asn	Leu	Val	Glu	Glu	Thr
				80					85					90

Ser	His	Phe	Val	Arg	Thr	Thr	Phe	Val	Ser	Arg	His	Lys	Lys	Phe
				95					100					105

Asp	Glu	Phe	Phe	Arg	Glu	Leu	Leu	Glu	Asn	Ala	Glu	Lys	Ser	Leu
				110					115					120

Asn	Asp	Met	Phe	Val	Arg	Thr	Tyr	Gly	Met	Leu	Tyr	Met	Gln	Asn
				125					130					135

Ser	Glu	Val	Phe	Gln	Asp	Leu	Phe	Thr	Glu	Leu	Lys	Arg	Tyr	Tyr
				140					145					150

Thr Gly Gly Asn Val Asn Leu Glu Glu Met Leu Asn Asp Phe Trp	155	160	165
Ala Arg Leu Leu Glu Arg Met Phe Gln Leu Ile Asn Pro Gln Tyr	170	175	180
His Phe Ser Glu Asp Tyr Leu Glu Cys Val Ser Lys Tyr Thr Asp	185	190	195
Gln Leu Lys Pro Phe Gly Asp Val Pro Arg Lys Leu Lys Ile Gln	200	205	210
Val Thr Arg Ala Phe Ile Ala Ala Arg Thr Phe Val Gln Gly Leu	215	220	225
Thr Val Gly Arg Glu Val Ala Asn Arg Val Ser Lys Val Ser Pro	230	235	240
Thr Pro Gly Cys Ile Arg Ala Leu Met Lys Met Leu Tyr Cys Pro	245	250	255
Tyr Cys Arg Gly Leu Pro Thr Val Arg Pro Cys Asn Asn Tyr Cys	260	265	270
Leu Asn Val Met Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp	275	280	285
Thr Glu Trp Asn Leu Phe Ile Asp Ala Met Leu Leu Val Ala Glu	290	295	300
Arg Leu Glu Gly Pro Phe Asn Ile Glu Ser Val Met Asp Pro Ile	305	310	315
Asp Val Lys Ile Ser Glu Ala Ile Met Asn Met Gln Glu Asn Ser	320	325	330
Met Gln Val Ser Ala Lys Val Phe Gln Gly Cys Gly Gln Pro Lys	335	340	345
Pro Ala Pro Ala Leu Arg Ser Ala Arg Ser Ala Pro Glu Asn Phe	350	355	360
Asn Thr Arg Phe Arg Pro Tyr Asn Pro Glu Glu Arg Pro Thr Thr	365	370	375
Ala Ala Gly Thr Ser Leu Asp Arg Leu Val Thr Asp Ile Lys Glu	380	385	390
Lys Leu Lys Leu Ser Lys Lys Val Trp Ser Ala Leu Pro Tyr Thr	395	400	405
Ile Cys Lys Asp Glu Ser Val Thr Ala Gly Thr Ser Asn Glu Glu	410	415	420
Glu Cys Trp Asn Gly His Ser Lys Ala Arg Tyr Leu Pro Glu Ile	425	430	435

Met	Asn	Asp	Gly	Leu	Thr	Asn	Gln	Ile	Asn	Asn	Pro	Glu	Val	Asp	
				440					445					450	
Val	Asp	Ile	Thr	Arg	Pro	Asp	Thr	Phe	Ile	Arg	Gln	Gln	Ile	Met	
				455					460					465	
Ala	Leu	Arg	Val	Met	Thr	Asn	Lys	Leu	Lys	Asn	Ala	Tyr	Asn	Gly	
				470					475					480	
Asn	Asp	Val	Asn	Phe	Gln	Asp	Thr	Ser	Asp	Glu	Ser	Ser	Gly	Ser	
				485					490					495	
Gly	Ser	Gly	Ser	Gly	Cys	Met	Asp	Asp	Val	Cys	Pro	Thr	Glu	Phe	
				500					505					510	
Glu	Phe	Val	Thr	Thr	Glu	Ala	Pro	Ala	Val	Asp	Pro	Asp	Arg	Arg	
				515					520					525	
Glu	Val	Asp	Ser	Ser	Ala	Ala	Gln	Arg	Gly	His	Ser	Leu	Leu	Ser	
				530					535					540	
Trp	Ser	Leu	Thr	Cys	Ile	Val	Leu	Ala	Leu	Gln	Arg	Leu	Cys	Arg	
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<220>  
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<400> 110  
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<210> 111  
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 <213> Artificial Sequence

<220>  
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<400> 111  
 tgcacagtct ctgcagtgcc cagg 24

<210> 112  
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 <212> DNA  
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<210> 113  
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<212> DNA  
<213> Homo sapiens

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cgccaactac gcaaagacca agcgggctcc gcgcggaccg gccgcggggc 150  
tagggacccg gctttggcct tcaggctccc tagcagcggg gaaaaggaat 200  
tgctgcccgg agtttctgcg gaggtggagg gagatcagga aacggcttct 250  
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<210> 114  
 <211> 515  
 <212> PRT  
 <213> Homo sapiens

<400> 114  
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 Gln Ala Cys Val Cys Pro Gly Lys Met Leu Ala Met Gly Ala Leu  
 20 25 30  
 Ala Gly Phe Trp Ile Leu Cys Leu Leu Thr Tyr Gly Tyr Leu Ser  
 35 40 45  
 Trp Gly Gln Ala Leu Glu Glu Glu Glu Gly Ala Leu Leu Ala  
 50 55 60  
 Gln Ala Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser Gln  
 65 70 75  
 Pro His Leu Ile Phe Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp  
 80 85 90  
 Val Gly Tyr His Gly Ser Glu Ile Lys Thr Pro Thr Leu Asp Lys  
 95 100 105  
 Leu Ala Ala Glu Gly Val Lys Leu Glu Asn Tyr Tyr Val Gln Pro  
 110 115 120  
 Ile Cys Thr Pro Ser Arg Ser Gln Phe Ile Thr Gly Lys Tyr Gln  
 125 130 135  
 Ile His Thr Gly Leu Gln His Ser Ile Ile Arg Pro Thr Gln Pro  
 140 145 150

Asn Cys Leu Pro Leu Asp Asn Ala Thr Leu Pro Gln Lys Leu Lys	155	160	165
Glu Val Gly Tyr Ser Thr His Met Val Gly Lys Trp His Leu Gly	170	175	180
Phe Asn Arg Lys Glu Cys Met Pro Thr Arg Arg Gly Phe Asp Thr	185	190	195
Phe Phe Gly Ser Leu Leu Gly Ser Gly Asp Tyr Tyr Thr His Tyr	200	205	210
Lys Cys Asp Ser Pro Gly Met Cys Gly Tyr Asp Leu Tyr Glu Asn	215	220	225
Asp Asn Ala Ala Trp Asp Tyr Asp Asn Gly Ile Tyr Ser Thr Gln	230	235	240
Met Tyr Thr Gln Arg Val Gln Gln Ile Leu Ala Ser His Asn Pro	245	250	255
Thr Lys Pro Ile Phe Leu Tyr Thr Ala Tyr Gln Ala Val His Ser	260	265	270
Pro Leu Gln Ala Pro Gly Arg Tyr Phe Glu His Tyr Arg Ser Ile	275	280	285
Ile Asn Ile Asn Arg Arg Arg Tyr Ala Ala Met Leu Ser Cys Leu	290	295	300
Asp Glu Ala Ile Asn Asn Val Thr Leu Ala Leu Lys Thr Tyr Gly	305	310	315
Phe Tyr Asn Asn Ser Ile Ile Ile Tyr Ser Ser Asp Asn Gly Gly	320	325	330
Gln Pro Thr Ala Gly Gly Ser Asn Trp Pro Leu Arg Gly Ser Lys	335	340	345
Gly Thr Tyr Trp Glu Gly Gly Ile Arg Ala Val Gly Phe Val His	350	355	360
Ser Pro Leu Leu Lys Asn Lys Gly Thr Val Cys Lys Glu Leu Val	365	370	375
His Ile Thr Asp Trp Tyr Pro Thr Leu Ile Ser Leu Ala Glu Gly	380	385	390
Gln Ile Asp Glu Asp Ile Gln Leu Asp Gly Tyr Asp Ile Trp Glu	395	400	405
Thr Ile Ser Glu Gly Leu Arg Ser Pro Arg Val Asp Ile Leu His	410	415	420
Asn Ile Asp Pro Tyr Thr Pro Arg Gln Lys Met Ala Pro Gly Gln	425	430	435

Gln	Ala	Met	Gly	Ser	Gly	Thr	Leu	Gln	Ser	Ser	Gln	Pro	Ser	Glu	440	445	450
Cys	Ser	Thr	Gly	Asn	Cys	Leu	Gln	Glu	Ile	Leu	Ala	Thr	Ala	Thr	455	460	465
Gly	Ser	Pro	Leu	Ser	Leu	Ser	Ala	Thr	Trp	Asp	Arg	Thr	Gly	Gly	470	475	480
Thr	Met	Asn	Gly	Ser	Pro	Cys	Gln	Leu	Ala	Lys	Val	Tyr	Gly	Phe	485	490	495
Ser	Thr	Ser	Gln	Pro	Thr	His	Met	Arg	Gly	Trp	Thr	Tyr	Leu	Thr	500	505	510
Gly	Ile	Gln	Glu	Ser											515		

<210> 115  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 115  
 cccaacccaa ctgtttacct ctgg 24

<210> 116  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 116  
 ctctctgagt gtacatctgt gtgg 24

<210> 117  
 <211> 53  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<220>  
 <221> unsure  
 <222> 33  
 <223> unknown base

<400> 117  
 gccaccctac ctcagaaact gaaggagggtt ggntattcaa cgcataatggt 50

cgg 53

<210> 118

<211> 2260

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2009, 2026, 2033, 2055, 2074, 2078, 2086

<223> unknown base

<400> 118

cggacgcgtg ggtgcgagtg gagcggagga cccgagcggc tgaggagaga 50  
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gggctcagga ggaggaagga ggacccgtgc gagaatgcct ctgccctgga 150  
gccttgcgct cccgctgctg ctctcctggg tggcaggtgg tttcgggaaac 200  
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ctctacccc taaggtgaac ttgcagccct tcaactatga agagatagtt 1100

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<210> 119

<211> 338

<212> PRT

<213> Homo sapiens

<400> 119

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Val	Ala	Gly	Gly	Phe	Gly	Asn	Ala	Ala	Ser	Ala	Arg	His	His	Gly	20	25	30
Leu	Leu	Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr	35	40	45
Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	50	55	60
Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	65	70	75
Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	80	85	90
Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	95	100	105
Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	110	115	120
Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	125	130	135
Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr	140	145	150
Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	155	160	165
Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	170	175	180
Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	185	190	195
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	200	205	210
Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	215	220	225
Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln	230	235	240
Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	245	250	255
Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	260	265	270
Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	275	280	285
His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	290	295	300

Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro  
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Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly  
320 325 330

Gly Lys Lys Gly Asn Glu Glu Lys  
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<210> 120

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 120

cctcagtggc cacatgctca tg 22

<210> 121

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 121

ggctgcacgt atggctatcc atag 24

<210> 122

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 122

gataaactgt cagtacagct gtgaagacac agaagaaggg ccacagtgcc 50

<210> 123

<211> 1199

<212> DNA

<213> Homo sapiens

<400> 123

gggagctgct gctgtggctg ctggtgctgt gcgcgctgct cctgctcttg 50

gtgcagctgc tgcgcttctt gagggctgac ggcgacctga cgctactatg 100

ggccgagtggt cagggacgac gcccagaatg ggagctgact gatatggtgg 150

tgtgggtgac tggagcctcg agtggaattg gtgaggagct ggcttaccag 200

ttgtctaaac taggagtttc tcttgtgctg tcagccagaa gagtgcata 250

gctggaaagg gtgaaaagaa gatgcctaga gaatggcaat ttaaaagaaa 300  
aagatatact tgttttgccc cttgacctga ccgacactgg ttcccatgaa 350  
gcggtacca aagctgttct ccaggagttt ggtagaatcg acattctggt 400  
caacaatggt ggaatgtccc agcgttctct gtgcatggat accagcttgg 450  
atgtctacag aaagctaata gagcttaact acttagggac ggtgtccttg 500  
acaaaatgtg ttctgcctca catgatcgag aggaagcaag gaaagattgt 550  
tactgtgaat agcatcctgg gtatcatatc tgtacctctt tccattggat 600  
actgtgctag caagcatgct ctccgggggt tttttaatgg ccttcgaaca 650  
gaacttgcca catacccagg tataatagtt tctaacattt gcccaggacc 700  
tgtgcaatca aatattgtgg agaattccct agctggagaa gtcacaaaga 750  
ctataggcaa taatggagac cagtcccaca agatgacaac cagtcgttgt 800  
gtgcggctga tgtaatcag catggccaat gatttgaaag aagtttggat 850  
ctcagaacaa cttttcttgt tagtaacata tttgtggcaa tacatgcaa 900  
cctgggcctg gtggataacc aacaagatgg ggaagaaaag gattgagaac 950  
tttaagagtg gtgtggatgc agactcttct tattttaaaa tctttaagac 1000  
aaaacatgac tgaaaagagc acctgtactt ttcaagccac tggagggaga 1050  
aatggaaaac atgaaaacag caatcttctt atgcttctga ataatcaaag 1100  
actaatttgt gattttactt tttaatagat atgactttgc ttccaacatg 1150  
gaatgaaata aaaaataaat aataaaagat tgccatgaat cttgcaaaa 1199

<210> 124

<211> 289

<212> PRT

<213> Homo sapiens

<400> 124

Met	Val	Val	Trp	Val	Thr	Gly	Ala	Ser	Ser	Gly	Ile	Gly	Glu	Glu
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Leu	Ala	Tyr	Gln	Leu	Ser	Lys	Leu	Gly	Val	Ser	Leu	Val	Leu	Ser
				20					25				30	

Ala	Arg	Arg	Val	His	Glu	Leu	Glu	Arg	Val	Lys	Arg	Arg	Cys	Leu
				35					40				45	

Glu	Asn	Gly	Asn	Leu	Lys	Glu	Lys	Asp	Ile	Leu	Val	Leu	Pro	Leu
				50					55				60	



Asp	Leu	Thr	Asp	Thr	Gly	Ser	His	Glu	Ala	Ala	Thr	Lys	Ala	Val	65	70	75
Leu	Gln	Glu	Phe	Gly	Arg	Ile	Asp	Ile	Leu	Val	Asn	Asn	Gly	Gly	80	85	90
Met	Ser	Gln	Arg	Ser	Leu	Cys	Met	Asp	Thr	Ser	Leu	Asp	Val	Tyr	95	100	105
Arg	Lys	Leu	Ile	Glu	Leu	Asn	Tyr	Leu	Gly	Thr	Val	Ser	Leu	Thr	110	115	120
Lys	Cys	Val	Leu	Pro	His	Met	Ile	Glu	Arg	Lys	Gln	Gly	Lys	Ile	125	130	135
Val	Thr	Val	Asn	Ser	Ile	Leu	Gly	Ile	Ile	Ser	Val	Pro	Leu	Ser	140	145	150
Ile	Gly	Tyr	Cys	Ala	Ser	Lys	His	Ala	Leu	Arg	Gly	Phe	Phe	Asn	155	160	165
Gly	Leu	Arg	Thr	Glu	Leu	Ala	Thr	Tyr	Pro	Gly	Ile	Ile	Val	Ser	170	175	180
Asn	Ile	Cys	Pro	Gly	Pro	Val	Gln	Ser	Asn	Ile	Val	Glu	Asn	Ser	185	190	195
Leu	Ala	Gly	Glu	Val	Thr	Lys	Thr	Ile	Gly	Asn	Asn	Gly	Asp	Gln	200	205	210
Ser	His	Lys	Met	Thr	Thr	Ser	Arg	Cys	Val	Arg	Leu	Met	Leu	Ile	215	220	225
Ser	Met	Ala	Asn	Asp	Leu	Lys	Glu	Val	Trp	Ile	Ser	Glu	Gln	Pro	230	235	240
Phe	Leu	Leu	Val	Thr	Tyr	Leu	Trp	Gln	Tyr	Met	Pro	Thr	Trp	Ala	245	250	255
Trp	Trp	Ile	Thr	Asn	Lys	Met	Gly	Lys	Lys	Arg	Ile	Glu	Asn	Phe	260	265	270
Lys	Ser	Gly	Val	Asp	Ala	Asp	Ser	Ser	Tyr	Phe	Lys	Ile	Phe	Lys	275	280	285

Thr Lys His Asp

<210> 125

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 125

gcaatgaact gggagctgc 19

<210> 126

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

ctgtgaatag catcctggg 19

<210> 127

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 127

cttttcaagc cactggagg 20

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 128

ctgtagacat ccaagctggt atcc 24

<210> 129

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 129

aagagtctgc atccacacca ctc 23

<210> 130

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 130

acctgacgct actatgggcc gagtggcagg gacgacgcc agaag 46

<210> 131  
<211> 2365  
<212> DNA  
<213> Homo sapiens

<400> 131  
gcgacgtggg caccgccatc agctgttcgc gcgtcttctc ctccaggtgg 50  
ggcaggggtt tcgggctggt ggagcatgtg ctgggacagg acagcatcct 100  
caatcaatcc aacagcatat tcggttgcac cttctacaca ctacagctat 150  
tgttaggttg cctgcggaca cgctgggcct ctgtcctgat gctgctgagc 200  
tccctggtgt ctctcgtcgtg ttctgtctac ctggcctgga tcctgttctt 250  
cgtgctctat gattttctgca ttgtttgtat caccacctat gctatcaacg 300  
tgagcctgat gtggctcagt ttccggaagg tccaagaacc ccagggcaag 350  
gctaagaggc actgagccct caaccaagc caggctgacc tcctctgctt 400  
tgctttggtc ttcaagccgc tcagcgtgcc tgtggacagc gtggccccgg 450  
ccccccaag cctcaggagg gcaacacagt ccctggcgag tggccctggc 500  
aggccagtgt gaggaggcaa ggagcccaca tctgcagcgg ctccctggtg 550  
gcagacacct gggctctcac tgctgcccac tgctttgaaa aggcagcagc 600  
aacagaactg aattcctggt cagtggctct gggttctctg cagcgtgagg 650  
gactcagccc tggggccgaa gaggtggggg tggctgccct gcagttgccc 700  
agggcctata accactacag ccagggtcca gacctggccc tgctgcagct 750  
cgcccccccc acgaccaca caccctctg cctgccccag cccgccatc 800  
gcttccccct tggagcctcc tgctgggcca ctggctggga tcaggacacc 850  
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ggccccctgtc agggagattc cgggggccct gtgctgtgcc tcgagcctga 1050  
cggacactgg gttcaggctg gcatcatcag ctttgcacatc agctgtgccc 1100  
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cccgagatg agtgatgagg acagctgtgt agcctgtgga tccttgagga 1250  
cagcaggtcc ccaggcagga gcaccctccc catggcctg ggaggccagg 1300

ctgatgcacc agggacagct ggcctgtggc ggagccctgg tgtcagagga 1350  
 ggcggtgcta actgctgccc actgcttcat tgggcgccag gcccagagg 1400  
 aatggagcgt agggctgggg accagaccgg aggagtgggg cctgaagcag 1450  
 ctcacctgc atggagccta caccaccct gaggggggct acgacatggc 1500  
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 gcccgtagcc ctctggggc ctagggcctg cagccggctg catgcagctc 1700  
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 cttgccaaagg ccccgccagg ccggcgggtct tcaccgcgct ccctgcctat 1900  
 gaggaactggg tcagcagttt ggactggcag gtctacttcg ccgaggaacc 1950  
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 tgttacaaaa taaaa 2365

<210> 132

<211> 571

<212> PRT

<213> Homo sapiens

<400> 132

Met	Leu	Leu	Ser	Ser	Leu	Val	Ser	Leu	Ala	Gly	Ser	Val	Tyr	Leu
1				5					10					15

Ala	Trp	Ile	Leu	Phe	Phe	Val	Leu	Tyr	Asp	Phe	Cys	Ile	Val	Cys
				20					25					30

Ile Thr Thr Tyr Ala	Ile Asn Val Ser	Leu Met Trp	Leu Ser Phe
35	40		45
Arg Lys Val Gln Glu	Pro Gln Gly Lys	Ala Lys Arg His	Gly Asn
50	55		60
Thr Val Pro Gly Glu	Trp Pro Trp Gln	Ala Ser Val Arg	Arg Gln
65	70		75
Gly Ala His Ile Cys	Ser Gly Ser Leu	Val Ala Asp Thr	Trp Val
80	85		90
Leu Thr Ala Ala His	Cys Phe Glu Lys	Ala Ala Ala Thr	Glu Leu
95	100		105
Asn Ser Trp Ser Val	Val Leu Gly Ser	Leu Gln Arg Glu	Gly Leu
110	115		120
Ser Pro Gly Ala Glu	Glu Val Gly Val	Ala Ala Leu Gln	Leu Pro
125	130		135
Arg Ala Tyr Asn His	Tyr Ser Gln Gly	Ser Asp Leu Ala	Leu Leu
140	145		150
Gln Leu Ala His Pro	Thr Thr His Thr	Pro Leu Cys Leu	Pro Gln
155	160		165
Pro Ala His Arg Phe	Pro Phe Gly Ala	Ser Cys Trp Ala	Thr Gly
170	175		180
Trp Asp Gln Asp Thr	Ser Asp Ala Pro	Gly Thr Leu Arg	Asn Leu
185	190		195
Arg Leu Arg Leu Ile	Ser Arg Pro Thr	Cys Asn Cys Ile	Tyr Asn
200	205		210
Gln Leu His Gln Arg	His Leu Ser Asn	Pro Ala Arg Pro	Gly Met
215	220		225
Leu Cys Gly Gly Pro	Gln Pro Gly Val	Gln Gly Pro Cys	Gln Gly
230	235		240
Asp Ser Gly Gly Pro	Val Leu Cys Leu	Glu Pro Asp Gly	His Trp
245	250		255
Val Gln Ala Gly Ile	Ile Ser Phe Ala	Ser Ser Cys Ala	Gln Glu
260	265		270
Asp Ala Pro Val Leu	Leu Thr Asn Thr	Ala Ala His Ser	Ser Trp
275	280		285
Leu Gln Ala Arg Val	Gln Gly Ala Ala	Phe Leu Ala Gln	Ser Pro
290	295		300
Glu Thr Pro Glu Met	Ser Asp Glu Asp	Ser Cys Val Ala	Cys Gly
305	310		315

Ser	Leu	Arg	Thr	Ala	Gly	Pro	Gln	Ala	Gly	Ala	Pro	Ser	Pro	Trp	
				320					325					330	
Pro	Trp	Glu	Ala	Arg	Leu	Met	His	Gln	Gly	Gln	Leu	Ala	Cys	Gly	
				335					340					345	
Gly	Ala	Leu	Val	Ser	Glu	Glu	Ala	Val	Leu	Thr	Ala	Ala	His	Cys	
				350					355					360	
Phe	Ile	Gly	Arg	Gln	Ala	Pro	Glu	Glu	Trp	Ser	Val	Gly	Leu	Gly	
				365					370					375	
Thr	Arg	Pro	Glu	Glu	Trp	Gly	Leu	Lys	Gln	Leu	Ile	Leu	His	Gly	
				380					385					390	
Ala	Tyr	Thr	His	Pro	Glu	Gly	Gly	Tyr	Asp	Met	Ala	Leu	Leu	Leu	
				395					400					405	
Leu	Ala	Gln	Pro	Val	Thr	Leu	Gly	Ala	Ser	Leu	Arg	Pro	Leu	Cys	
				410					415					420	
Leu	Pro	Tyr	Pro	Asp	His	His	Leu	Pro	Asp	Gly	Glu	Arg	Gly	Trp	
				425					430					435	
Val	Leu	Gly	Arg	Ala	Arg	Pro	Gly	Ala	Gly	Ile	Ser	Ser	Leu	Gln	
				440					445					450	
Thr	Val	Pro	Val	Thr	Leu	Leu	Gly	Pro	Arg	Ala	Cys	Ser	Arg	Leu	
				455					460					465	
His	Ala	Ala	Pro	Gly	Gly	Asp	Gly	Ser	Pro	Ile	Leu	Pro	Gly	Met	
				470					475					480	
Val	Cys	Thr	Ser	Ala	Val	Gly	Glu	Leu	Pro	Ser	Cys	Glu	Gly	Leu	
				485					490					495	
Ser	Gly	Ala	Pro	Leu	Val	His	Glu	Val	Arg	Gly	Thr	Trp	Phe	Leu	
				500					505					510	
Ala	Gly	Leu	His	Ser	Phe	Gly	Asp	Ala	Cys	Gln	Gly	Pro	Ala	Arg	
				515					520					525	
Pro	Ala	Val	Phe	Thr	Ala	Leu	Pro	Ala	Tyr	Glu	Asp	Trp	Val	Ser	
				530					535					540	
Ser	Leu	Asp	Trp	Gln	Val	Tyr	Phe	Ala	Glu	Glu	Pro	Glu	Pro	Glu	
				545					550					555	
Ala	Glu	Pro	Gly	Ser	Cys	Leu	Ala	Asn	Ile	Ser	Gln	Pro	Thr	Ser	
				560					565					570	

Cys

<210> 133

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 133

cctgtgctgt gcctcgagcc tgac 24

<210> 134

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134

gtgggcagca gttagcaccg cctc 24

<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 135

ggctggcatc atcagctttg catcaagctg tgcccaggag gacgc 45

<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 136

cgggccgccc ccggcccca ttggggccgg gcctcgctgc ggcggcgact 50  
gagccaggct gggccgcgtc cctgagtccc agagtcggcg cggcgcgga 100  
ggggcagcct tccaccacgg ggagcccagc tgtcagccgc ctcacaggaa 150  
gatgtgctg cggcggggca gccctggcat ggggtgtgcat gtgggtgcag 200  
ccctgggagc actgtggttc tgcctcacag gagccctgga ggtccaggtc 250  
cctgaagacc cagtgggtggc actgggtggc accgatgcca ccctgtgctg 300  
ctcctttctcc cctgagcctg gcttcagcct ggcacagctc aacctcatct 350  
ggcagctgac agatacaaaa cagctgggtgc acagctttgc tgagggccag 400  
gaccagggca ggccttatgc caaccgcacg gccctcttcc cggacctgct 450  
ggcacagggc aacgcatecc tgaggctgca gcgcgtgctg gtggcggacg 500  
agggcagctt cacctgcttc gtgagcatcc gggatttcgg cagcgctgcc 550

gtcagcctgc aggtggccgc tccctactcg aagcccagca tgaccctgga 600  
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gctaccaggg ctaccctgag gctgaggtgt tctggcagga tgggcagggt 700  
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cctacagctg cctggtgcgc aaccccgtgc tgcagcagga tgcgcacrgc 850  
tctgtcacca tcacaggga gcctatgaca ttccccccag aggccctgtg 900  
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tccaatggcc gtgatacact agtgatcatg ttcagccctg cttccacctg 1600  
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gcctctggcc agctcctggc ctctggtaga gtgagacttc agacgttctg 1850  
atgccttccg gatgtcatct ctccctgccc caggaatgga agatgtgagg 1900  
acttctaatt taaatgtggg actcggaggg attttgtaaa ctgggggtat 1950



attttgggga aaataaatgt ctttgtaaaa aaaaaaaaaa aaaaaaaaa 1998

<210> 137

<211> 316

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 233

<223> unknown amino acid

<400> 137

Met	Leu	Arg	Arg	Arg	Gly	Ser	Pro	Gly	Met	Gly	Val	His	Val	Gly	
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Ala	Ala	Leu	Gly	Ala	Leu	Trp	Phe	Cys	Leu	Thr	Gly	Ala	Leu	Glu	
				20					25					30	
Val	Gln	Val	Pro	Glu	Asp	Pro	Val	Val	Ala	Leu	Val	Gly	Thr	Asp	
				35					40					45	
Ala	Thr	Leu	Cys	Cys	Ser	Phe	Ser	Pro	Glu	Pro	Gly	Phe	Ser	Leu	
				50					55					60	
Ala	Gln	Leu	Asn	Leu	Ile	Trp	Gln	Leu	Thr	Asp	Thr	Lys	Gln	Leu	
				65					70					75	
Val	His	Ser	Phe	Ala	Glu	Gly	Gln	Asp	Gln	Gly	Ser	Ala	Tyr	Ala	
				80					85					90	
Asn	Arg	Thr	Ala	Leu	Phe	Pro	Asp	Leu	Leu	Ala	Gln	Gly	Asn	Ala	
				95					100					105	
Ser	Leu	Arg	Leu	Gln	Arg	Val	Arg	Val	Ala	Asp	Glu	Gly	Ser	Phe	
				110					115					120	
Thr	Cys	Phe	Val	Ser	Ile	Arg	Asp	Phe	Gly	Ser	Ala	Ala	Val	Ser	
				125					130					135	
Leu	Gln	Val	Ala	Ala	Pro	Tyr	Ser	Lys	Pro	Ser	Met	Thr	Leu	Glu	
				140					145					150	
Pro	Asn	Lys	Asp	Leu	Arg	Pro	Gly	Asp	Thr	Val	Thr	Ile	Thr	Cys	
				155					160					165	
Ser	Ser	Tyr	Gln	Gly	Tyr	Pro	Glu	Ala	Glu	Val	Phe	Trp	Gln	Asp	
				170					175					180	
Gly	Gln	Gly	Val	Pro	Leu	Thr	Gly	Asn	Val	Thr	Thr	Ser	Gln	Met	
				185					190					195	
Ala	Asn	Glu	Gln	Gly	Leu	Phe	Asp	Val	His	Ser	Val	Leu	Arg	Val	
				200					205					210	
Val	Leu	Gly	Ala	Asn	Gly	Thr	Tyr	Ser	Cys	Leu	Val	Arg	Asn	Pro	
				215					220					225	

Val	Leu	Gln	Gln	Asp	Ala	His	Xaa	Ser	Val	Thr	Ile	Thr	Gly	Gln
				230					235					240
Pro	Met	Thr	Phe	Pro	Pro	Glu	Ala	Leu	Trp	Val	Thr	Val	Gly	Leu
				245					250					255
Ser	Val	Cys	Leu	Ile	Ala	Leu	Leu	Val	Ala	Leu	Ala	Phe	Val	Cys
				260					265					270
Trp	Arg	Lys	Ile	Lys	Gln	Ser	Cys	Glu	Glu	Glu	Asn	Ala	Gly	Ala
				275					280					285
Glu	Asp	Gln	Asp	Gly	Glu	Gly	Glu	Gly	Ser	Lys	Thr	Ala	Leu	Gln
				290					295					300
Pro	Leu	Lys	His	Ser	Asp	Ser	Lys	Glu	Asp	Asp	Gly	Gln	Glu	Ile
				305					310					315

Ala

<210> 138  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 138  
 ctggcacagc tcaacctcat ctgg 24

<210> 139  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 139  
 gctgtctgtc tgtctcattg 20

<210> 140  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 140  
 ggacacagta tactgaccac 20

<210> 141  
 <211> 24

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 141  
tgcgaaccag gcagctgtaa gtgc 24

<210> 142  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 142  
tggaagaaga ggggtggtgat gtgg 24

<210> 143  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 143  
cagctgacag acaccaaaca gctggtgcac agtttcaccg aaggc 45

<210> 144  
<211> 2336  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1620, 1673  
<223> unknown base

<400> 144  
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gaagggggag tcctgaactt gtctgaagcc cttgtccgta agccttgaac 100  
tacgttctta aatctatgaa gtcgaggac ctttcgctgc tttttagagg 150  
acttctttcc ttgcttcagc aacatgaggc ttttcttggtg gaacgcggtc 200  
ttgactctgt tcgtcacttc tttgattggg gctttgatcc ctgaaccaga 250  
agtgaaaatt gaagtctcc agaagccatt catctgccat cgcaagacca 300  
aaggagggga tttgatgttg gtccactatg aaggctactt agaaaaggac 350  
ggctccttat ttcactccac tcacaaacat aacaatggtc agcccatttg 400

gtttaccctg ggcacacctg aggtctctcaa aggttgggac cagggcttga 450  
aaggaatgtg tgtaggagag aagagaaagc tcatcattcc tcctgctctg 500  
ggctatggaa aagaaggaaa aggtaaaatt cccccagaaa gtacactgat 550  
atttaatat gatctcctgg agattcgaaa tggaccaaga tcccatgaat 600  
cattccaaga aatggatctt aatgatgact ggaaactctc taaagatgag 650  
gttaaagcat atttaaagaa ggagtttgaa aaacatgggtg cgggtggtgaa 700  
tgaaagtcac catgatgctt tgggtggagga tatttttgat aaagaagatg 750  
aagacaaaaga tgggtttata tctgccagag aatttacata taaacacgat 800  
gagttataga gatacatcta cccttttaac atagcactca tctttcaaga 850  
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 tgtctctact aaaaatacaa aaattagcca ggcgtggtgg tgcacacctg 2150  
 tagtcccagc tactcgggag gctgagacag gagatttgct tgaacccggg 2200  
 aggcgagggt tgcagtgagc caagattgtg ccaactgcact ccagcctggg 2250  
 tgacagagca agactccatc tcaaaaaaaaa aaaaaagaag cagacctaca 2300  
 gcagctacta ttgaataaat acctatcctg gatattt 2336

<210> 145

<211> 211

<212> PRT

<213> Homo sapiens

<400> 145

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			20						25					30
Val	Leu	Gln	Lys	Pro	Phe	Ile	Cys	His	Arg	Lys	Thr	Lys	Gly	Gly
			35						40					45
Asp	Leu	Met	Leu	Val	His	Tyr	Glu	Gly	Tyr	Leu	Glu	Lys	Asp	Gly
			50						55					60
Ser	Leu	Phe	His	Ser	Thr	His	Lys	His	Asn	Asn	Gly	Gln	Pro	Ile
			65						70					75
Trp	Phe	Thr	Leu	Gly	Ile	Leu	Glu	Ala	Leu	Lys	Gly	Trp	Asp	Gln
			80						85					90
Gly	Leu	Lys	Gly	Met	Cys	Val	Gly	Glu	Lys	Arg	Lys	Leu	Ile	Ile
			95						100					105
Pro	Pro	Ala	Leu	Gly	Tyr	Gly	Lys	Glu	Gly	Lys	Gly	Lys	Ile	Pro
			110						115					120
Pro	Glu	Ser	Thr	Leu	Ile	Phe	Asn	Ile	Asp	Leu	Leu	Glu	Ile	Arg
			125						130					135
Asn	Gly	Pro	Arg	Ser	His	Glu	Ser	Phe	Gln	Glu	Met	Asp	Leu	Asn
			140						145					150

Asp	Asp	Trp	Lys	Leu	Ser	Lys	Asp	Glu	Val	Lys	Ala	Tyr	Leu	Lys
				155					160					165
Lys	Glu	Phe	Glu	Lys	His	Gly	Ala	Val	Val	Asn	Glu	Ser	His	His
				170					175					180
Asp	Ala	Leu	Val	Glu	Asp	Ile	Phe	Asp	Lys	Glu	Asp	Glu	Asp	Lys
				185					190					195
Asp	Gly	Phe	Ile	Ser	Ala	Arg	Glu	Phe	Thr	Tyr	Lys	His	Asp	Glu
				200					205					210

Leu

<210> 146

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 146

ctttccttgcc ttcagcaaca tgaggc 26

<210> 147

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 147

gcccagagca ggaggaatga tgagc 25

<210> 148

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 148

gtggaacgcg gtcttgactc tgttcgtcac ttctttgatt ggggctttg 49

<210> 149

<211> 2196

<212> DNA

<213> Homo sapiens

<400> 149

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tttttttagc atccaaccat tcctcccttg tagttctcgc cccctcaa 100  
caccctctcc cgtagcccac ccgactaaca tctcagtctc tgaaaatgca 150  
cagagatgcc tggctacctc gccctgcctt cagcctcagc gggctcagtc 200  
tctttttctc tttggtgcc aaggacgga gcatggaggt cacagtacct 250  
gccaccctca acgtcctcaa tggctctgac gcccgcctgc cctgcacctt 300  
caactcctgc tacacagtga accacaaaca gttctccctg aactggactt 350  
accaggagtg caacaactgc tctgaggaga tggtcctcca gttccgcatg 400  
aagatcatta acctgaagct ggagcgggtt caagaccgcg tggagttctc 450  
aggaacccc agcaagtacg atgtgtcggg gatgctgaga aacgtgcagc 500  
cggaggatga ggggatttac aactgctaca tcatgaacct ccctgaccgc 550  
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caagacggac ggtgaaggca acccgatga tggcgccaag tagtgggtgg 800  
ccggccctgc agcctcccgt gtccgtctc ctcccctctc cgccctgtac 850  
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agggccacc tggggcctcc tgaacccccg acttcgtatc tcccaccctg 950  
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gacgtgtggg ccctggggag aggagagaaa gggctccac ctgccagtcc 1050  
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ataaggggag gccttgaac ctgagctgcc aatgccagcc ctgtcccatc 1850  
tgcgggccacg ctactcgctc ctctcccaac aactcccttc gtggggacaa 1900  
aagtgacaat ttagggccag gcacagtggc tcacgcctgt aatcccagca 1950  
ctttgggagg ccaaggcggg tggattacct ccatctgttt agtagaaatg 2000  
ggcaaaaccc catctctact aaaaatacaa gaattagctg ggcgtgggtg 2050  
cgtgtgcctg taatcccagc tatttgggag gctgaggcag gagaatcgct 2100  
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tgcaattcag cctgggtgac atagagagac tccatctcaa aaaaaa 2196

<210> 150  
<211> 215  
<212> PRT  
<213> Homo sapiens

<400> 150  
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Gly Leu Ser Leu Phe Phe Ser Leu Val Pro Pro Gly Arg Ser Met  
20 25 30  
Glu Val Thr Val Pro Ala Thr Leu Asn Val Leu Asn Gly Ser Asp  
35 40 45  
Ala Arg Leu Pro Cys Thr Phe Asn Ser Cys Tyr Thr Val Asn His  
50 55 60  
Lys Gln Phe Ser Leu Asn Trp Thr Tyr Gln Glu Cys Asn Asn Cys  
65 70 75  
Ser Glu Glu Met Phe Leu Gln Phe Arg Met Lys Ile Ile Asn Leu  
80 85 90  
Lys Leu Glu Arg Phe Gln Asp Arg Val Glu Phe Ser Gly Asn Pro  
95 100 105  
Ser Lys Tyr Asp Val Ser Val Met Leu Arg Asn Val Gln Pro Glu



110										115				120				
Asp	Glu	Gly	Ile	Tyr	Asn	Cys	Tyr	Ile	Met	Asn	Pro	Pro	Asp	Arg				
				125					130					135				
His	Arg	Gly	His	Gly	Lys	Ile	His	Leu	Gln	Val	Leu	Met	Glu	Glu				
				140					145					150				
Pro	Pro	Glu	Arg	Asp	Ser	Thr	Val	Ala	Val	Ile	Val	Gly	Ala	Ser				
				155					160					165				
Val	Gly	Gly	Phe	Leu	Ala	Val	Val	Ile	Leu	Val	Leu	Met	Val	Val				
				170					175					180				
Lys	Cys	Val	Arg	Arg	Lys	Lys	Glu	Gln	Lys	Leu	Ser	Thr	Asp	Asp				
				185					190					195				
Leu	Lys	Thr	Glu	Glu	Glu	Gly	Lys	Thr	Asp	Gly	Glu	Gly	Asn	Pro				
				200					205					210				
Asp	Asp	Gly	Ala	Lys														
				215														

<210> 151  
 <211> 524  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 103, 233  
 <223> unknown base

<400> 151  
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 tcctcccttg tagttctcgc cccctcaaat caccttctcc cttagcccac 100  
 ccnactaaca tctcagtctc tgaaaatgca cagagatgcc tggctacctc 150  
 gccctgcctt cagcctcacg gggtcagtc tctttttctc tttggtgcca 200  
 ccaggacgga gcatggaggt ccacagtacc tgnccaccct caacgtcctc 250  
 aatggctctg acgcccgcct gccctgcct tcaactcctg ctacacagtg 300  
 aaccacaaac agttctccct gaactggact taccaggagt gcaacaactg 350  
 ctctgaggag atgttctctc agttccgcat gaagatcatt aacctgaagc 400  
 tggagcggtt tcaagaccgc gtggagttct cagggaaccc cagcaagtac 450  
 gatgtgtcgg tgatgctgag aaacgtgcag ccggaggatg aggggattta 500  
 caactgctac atcatgaacc cccc 524

<210> 152

<211> 368  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 56, 123  
<223> unknown base

<400> 152  
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cctgccctgc accttcaact ccngctacac agtgaaccac aaacagttct 150  
  
ccctgaactg gatttaccag gagtgaaca actggctctg aggagatgtt 200  
  
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tcggtgatgc tgagaaacgt gcagccggag gatgagggga tttacaactg 350  
  
ctacatcatg aaccccc 368

<210> 153  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 153  
acggagcatg gaggtccaca gtac 24

<210> 154  
<211> 23  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 154  
gcacgtttct cagcatcacc gac 23

<210> 155  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 155

cgctgcct gcacctcaa ctctgctac acagtgaacc acaaacagtt 50

<210> 156

<211> 2680

<212> DNA

<213> Homo sapiens

<400> 156

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cgccggaccca gcgctcccg cggacgtca cccccagtg gtgctggctcc 150  
ctggtgattt gggtaaccaa ctggaagcca agctggacaa gccgacagtg 200  
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atgctgtaaa aaaaaaaaaa aaaaaaaaaa 2680

<210> 157

<211> 412

<212> PRT

<213> Homo Sapien

<400> 157

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				20					25					30	
Ala	Leu	Pro	Ala	Gly	Arg	His	Pro	Pro	Val	Val	Leu	Val	Pro	Gly	
				35					40					45	
Asp	Leu	Gly	Asn	Gln	Leu	Glu	Ala	Lys	Leu	Asp	Lys	Pro	Thr	Val	
				50					55					60	
Val	His	Tyr	Leu	Cys	Ser	Lys	Lys	Thr	Glu	Ser	Tyr	Phe	Thr	Ile	
				65					70					75	
Trp	Leu	Asn	Leu	Glu	Leu	Leu	Leu	Pro	Val	Ile	Ile	Asp	Cys	Trp	
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Ile	Asp	Asn	Ile	Arg	Leu	Val	Tyr	Asn	Lys	Thr	Ser	Arg	Ala	Thr	
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Gln	Phe	Pro	Asp	Gly	Val	Asp	Val	Arg	Val	Pro	Gly	Phe	Gly	Lys	
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Thr	Phe	Ser	Leu	Glu	Phe	Leu	Asp	Pro	Ser	Lys	Ser	Ser	Val	Gly	
				125					130					135	
Ser	Tyr	Phe	His	Thr	Met	Val	Glu	Ser	Leu	Val	Gly	Trp	Gly	Tyr	
				140					145					150	
Thr	Arg	Gly	Glu	Asp	Val	Arg	Gly	Ala	Pro	Tyr	Asp	Trp	Arg	Arg	
				155					160					165	
Ala	Pro	Asn	Glu	Asn	Gly	Pro	Tyr	Phe	Leu	Ala	Leu	Arg	Glu	Met	
				170					175					180	
Ile	Glu	Glu	Met	Tyr	Gln	Leu	Tyr	Gly	Gly	Pro	Val	Val	Leu	Val	
				185					190					195	
Ala	His	Ser	Met	Gly	Asn	Met	Tyr	Thr	Leu	Tyr	Phe	Leu	Gln	Arg	
				200					205					210	
Gln	Pro	Gln	Ala	Trp	Lys	Asp	Lys	Tyr	Ile	Arg	Ala	Phe	Val	Ser	
				215					220					225	
Leu	Gly	Ala	Pro	Trp	Gly	Gly	Val	Ala	Lys	Thr	Leu	Arg	Val	Leu	
				230					235					240	
Ala	Ser	Gly	Asp	Asn	Asn	Arg	Ile	Pro	Val	Ile	Gly	Pro	Leu	Lys	

245	250	255
Ile Arg Glu Gln Gln Arg Ser Ala Val	Ser Thr Ser Trp Leu Leu	
260	265	270
Pro Tyr Asn Tyr Thr Trp Ser Pro Glu	Lys Val Phe Val Gln Thr	
275	280	285
Pro Thr Ile Asn Tyr Thr Leu Arg Asp	Tyr Arg Lys Phe Phe Gln	
290	295	300
Asp Ile Gly Phe Glu Asp Gly Trp Leu	Met Arg Gln Asp Thr Glu	
305	310	315
Gly Leu Val Glu Ala Thr Met Pro Pro	Gly Val Gln Leu His Cys	
320	325	330
Leu Tyr Gly Thr Gly Val Pro Thr Pro	Asp Ser Phe Tyr Tyr Glu	
335	340	345
Ser Phe Pro Asp Arg Asp Pro Lys Ile	Cys Phe Gly Asp Gly Asp	
350	355	360
Gly Thr Val Asn Leu Lys Ser Ala Leu	Gln Cys Gln Ala Trp Gln	
365	370	375
Ser Arg Gln Glu His Gln Val Leu Leu	Gln Glu Leu Pro Gly Ser	
380	385	390
Glu His Ile Glu Met Leu Ala Asn Ala	Thr Thr Leu Ala Tyr Leu	
395	400	405
Lys Arg Val Leu Leu Gly Pro		
410		

<210> 158

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 158

ctggggctac acacggggtg agg 23

<210> 159

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 159

ggtgccgctg cagaaagtag agcg 24

<210> 160  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 160  
gccccaaatg aaaacgggcc ctacttcctg gccctccgcg agatg 45

<210> 161  
<211> 1512  
<212> DNA  
<213> Homo sapiens

<400> 161  
cggacgcgtg ggcggacgcg tggggcggcg gcagcggcgg cgacggcgac 50  
atggagagcg gggcctacgg cgcggccaag gcgggcggct ccttcgacct 100  
gcggcgcttc ctgacgcagc cgcagggtgtt ggcgcgcgcc gtgtgcttgg 150  
tcttcgcctt gatcgtgttc tctgcatct atggtgaggg ctacagcaat 200  
gccacgagt ctaagcagat gtactgcgtg ttcaaccgca acgaggatgc 250  
ctgccgctat ggcagtgcca tcgggggtgtt ggccttcctg gcctcggcct 300  
tcttcttgggt ggtcgacgcg tatttcccc agatcagcaa cgccactgac 350  
cgcaagtacc tggtcattgg tgacctgctc ttctcagctc tctggacctt 400  
cctgtggttt gttggtttct gcttcctcac caaccagtgg gcagtcacca 450  
acccgaagga cgtgctggtg ggggcccact ctgtgagggc agccatcacc 500  
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ccactccgga ccccaacact gcctacgcct cctaccaggg tgcattctgtg 650  
gacaactacc aacagccacc cttcacccag aacgcggaga ccaccgaggg 700  
ctaccagccg cccctgtgt actgagtggc ggtagcgtg ggaaggggga 750  
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ctgccagccc ctctctttca cctgttccat cctgtgcagc tgacacacag 850  
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ccgcctgcag tggctagaag ccagcaggtg cccatgtgct actgacaagt 1050  
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 gcgttctctg ccaaagactc gtggggggcca tcacacctgc cctgtgcagc 1150  
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 gtgccccatg gctcccagac tctgtctgtg ccgagtgtat tataaaatcg 1450  
 tgggggagat gcccggcctg ggatgctggt tggagacgga ataaatgttt 1500  
 tctcattcaa ag 1512

<210> 162

<211> 224

<212> PRT

<213> Homo sapiens

<400> 162

Met	Glu	Ser	Gly	Ala	Tyr	Gly	Ala	Ala	Lys	Ala	Gly	Gly	Ser	Phe	1	5	10	15
Asp	Leu	Arg	Arg	Phe	Leu	Thr	Gln	Pro	Gln	Val	Val	Ala	Arg	Ala	20	25	30	
Val	Cys	Leu	Val	Phe	Ala	Leu	Ile	Val	Phe	Ser	Cys	Ile	Tyr	Gly	35	40	45	
Glu	Gly	Tyr	Ser	Asn	Ala	His	Glu	Ser	Lys	Gln	Met	Tyr	Cys	Val	50	55	60	
Phe	Asn	Arg	Asn	Glu	Asp	Ala	Cys	Arg	Tyr	Gly	Ser	Ala	Ile	Gly	65	70	75	
Val	Leu	Ala	Phe	Leu	Ala	Ser	Ala	Phe	Phe	Leu	Val	Val	Asp	Ala	80	85	90	
Tyr	Phe	Pro	Gln	Ile	Ser	Asn	Ala	Thr	Asp	Arg	Lys	Tyr	Leu	Val	95	100	105	
Ile	Gly	Asp	Leu	Leu	Phe	Ser	Ala	Leu	Trp	Thr	Phe	Leu	Trp	Phe	110	115	120	
Val	Gly	Phe	Cys	Phe	Leu	Thr	Asn	Gln	Trp	Ala	Val	Thr	Asn	Pro	125	130	135	
Lys	Asp	Val	Leu	Val	Gly	Ala	Asp	Ser	Val	Arg	Ala	Ala	Ile	Thr	140	145	150	



Phe	Ser	Phe	Phe	Ser	Ile	Phe	Ser	Trp	Gly	Val	Leu	Ala	Ser	Leu
				155					160					165
Ala	Tyr	Gln	Arg	Tyr	Lys	Ala	Gly	Val	Asp	Asp	Phe	Ile	Gln	Asn
				170					175					180
Tyr	Val	Asp	Pro	Thr	Pro	Asp	Pro	Asn	Thr	Ala	Tyr	Ala	Ser	Tyr
				185					190					195
Pro	Gly	Ala	Ser	Val	Asp	Asn	Tyr	Gln	Gln	Pro	Pro	Phe	Thr	Gln
				200					205					210
Asn	Ala	Glu	Thr	Thr	Glu	Gly	Tyr	Gln	Pro	Pro	Pro	Val	Tyr	
				215					220					

<210> 163

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 163

tggtcttcgc cttgatcgtg ttct 24

<210> 164

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 164

gtgtactgag cggcggtag 20

<210> 165

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 165

ctgaaggaga tggctgccct cac 23

<210> 166

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 166  
ccaggaggct catgggaaag tcc 23

<210> 167  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 167  
ccacgagtct aagcagatgt actgcgtggt caaccgcaac gaggatgcct 50

<210> 168  
<211> 3143  
<212> DNA  
<213> Homo sapiens

<400> 168  
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agggtgatca gtgagcagaa ggatgcccgt ggccgaggcc ccccagggtg 100  
ctggcgggca gggggacgga ggtgatggcg aggaagcgga gccagagggg 150  
atgttcaagg cctgtgagga ctccaagaga aaagcccggg gctacctccg 200  
cctggtgccc ctgtttgtgc tgctggccct gctcgtgctg gcttcggcgg 250  
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tcttaccgcg cggaatcta gtgccttccg cagtgaacc gccaaagccc 400  
agaagatgct caaggagctc atcaccagca cccgcctggg aacttactac 450  
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 tttggaataa agctgcctga tcaaaaaaaaa aaaaaaaaaa aaa 3143

<210> 169

<211> 802

<212> PRT

<213> Homo sapiens

<400> 169

Met	Pro	Val	Ala	Glu	Ala	Pro	Gln	Val	Ala	Gly	Gly	Gln	Gly	Asp
1				5						10				15

Gly	Gly	Asp	Gly	Glu	Glu	Ala	Glu	Pro	Glu	Gly	Met	Phe	Lys	Ala
			20						25					30

Cys	Glu	Asp	Ser	Lys	Arg	Lys	Ala	Arg	Gly	Tyr	Leu	Arg	Leu	Val
				35					40					45

Pro	Leu	Phe	Val	Leu	Leu	Ala	Leu	Leu	Val	Leu	Ala	Ser	Ala	Gly
				50					55					60

Val	Leu	Leu	Trp	Tyr	Phe	Leu	Gly	Tyr	Lys	Ala	Glu	Val	Met	Val
				65					70					75

Ser	Gln	Val	Tyr	Ser	Gly	Ser	Leu	Arg	Val	Leu	Asn	Arg	His	Phe
				80					85					90

Ser	Gln	Asp	Leu	Thr	Arg	Arg	Glu	Ser	Ser	Ala	Phe	Arg	Ser	Glu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

95	100	105
Thr Ala Lys Ala Gln Lys Met Leu Lys	Glu Leu Ile Thr Ser Thr	
110	115	120
Arg Leu Gly Thr Tyr Tyr Asn Ser Ser	Ser Val Tyr Ser Phe Gly	
125	130	135
Glu Gly Pro Leu Thr Cys Phe Phe Trp	Phe Ile Leu Gln Ile Pro	
140	145	150
Glu His Arg Arg Leu Met Leu Ser Pro	Glu Val Val Gln Ala Leu	
155	160	165
Leu Val Glu Glu Leu Leu Ser Thr Val	Asn Ser Ser Ala Ala Val	
170	175	180
Pro Tyr Arg Ala Glu Tyr Glu Val Asp	Pro Glu Gly Leu Val Ile	
185	190	195
Leu Glu Ala Ser Val Lys Asp Ile Ala	Ala Leu Asn Ser Thr Leu	
200	205	210
Gly Cys Tyr Arg Tyr Ser Tyr Val Gly	Gln Gly Gln Val Leu Arg	
215	220	225
Leu Lys Gly Pro Asp His Leu Ala Ser	Ser Cys Leu Trp His Leu	
230	235	240
Gln Gly Pro Lys Asp Leu Met Leu Lys	Leu Arg Leu Glu Trp Thr	
245	250	255
Leu Ala Glu Cys Arg Asp Arg Leu Ala	Met Tyr Asp Val Ala Gly	
260	265	270
Pro Leu Glu Lys Arg Leu Ile Thr Ser	Val Tyr Gly Cys Ser Arg	
275	280	285
Gln Glu Pro Val Val Glu Val Leu Ala	Ser Gly Ala Ile Met Ala	
290	295	300
Val Val Trp Lys Lys Gly Leu His Ser	Tyr Tyr Asp Pro Phe Val	
305	310	315
Leu Ser Val Gln Pro Val Val Phe Gln	Ala Cys Glu Val Asn Leu	
320	325	330
Thr Leu Asp Asn Arg Leu Asp Ser Gln	Gly Val Leu Ser Thr Pro	
335	340	345
Tyr Phe Pro Ser Tyr Tyr Ser Pro Gln	Thr His Cys Ser Trp His	
350	355	360
Leu Thr Val Pro Ser Leu Asp Tyr Gly	Leu Ala Leu Trp Phe Asp	
365	370	375
Ala Tyr Ala Leu Arg Arg Gln Lys Tyr	Asp Leu Pro Cys Thr Gln	

380	385	390
Gly Gln Trp Thr Ile Gln Asn Arg Arg	Leu Cys Gly Leu Arg	Ile
395	400	405
Leu Gln Pro Tyr Ala Glu Arg Ile Pro Val Val Ala Thr Ala		Gly
410	415	420
Ile Thr Ile Asn Phe Thr Ser Gln Ile Ser Leu Thr Gly Pro Gly		
425	430	435
Val Arg Val His Tyr Gly Leu Tyr Asn Gln Ser Asp Pro Cys Pro		
440	445	450
Gly Glu Phe Leu Cys Ser Val Asn Gly Leu Cys Val Pro Ala Cys		
455	460	465
Asp Gly Val Lys Asp Cys Pro Asn Gly Leu Asp Glu Arg Asn Cys		
470	475	480
Val Cys Arg Ala Thr Phe Gln Cys Lys Glu Asp Ser Thr Cys Ile		
485	490	495
Ser Leu Pro Lys Val Cys Asp Gly Gln Pro Asp Cys Leu Asn Gly		
500	505	510
Ser Asp Glu Glu Gln Cys Gln Glu Gly Val Pro Cys Gly Thr Phe		
515	520	525
Thr Phe Gln Cys Glu Asp Arg Ser Cys Val Lys Lys Pro Asn Pro		
530	535	540
Gln Cys Asp Gly Arg Pro Asp Cys Arg Asp Gly Ser Asp Glu Glu		
545	550	555
His Cys Asp Cys Gly Leu Gln Gly Pro Ser Ser Arg Ile Val Gly		
560	565	570
Gly Ala Val Ser Ser Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu		
575	580	585
Gln Val Arg Gly Arg His Ile Cys Gly Gly Ala Leu Ile Ala Asp		
590	595	600
Arg Trp Val Ile Thr Ala Ala His Cys Phe Gln Glu Asp Ser Met		
605	610	615
Ala Ser Thr Val Leu Trp Thr Val Phe Leu Gly Lys Val Trp Gln		
620	625	630
Asn Ser Arg Trp Pro Gly Glu Val Ser Phe Lys Val Ser Arg Leu		
635	640	645
Leu Leu His Pro Tyr His Glu Glu Asp Ser His Asp Tyr Asp Val		
650	655	660
Ala Leu Leu Gln Leu Asp His Pro Val Val Arg Ser Ala Ala Val		

665	670	675
Arg Pro Val Cys Leu Pro Ala Arg Ser	His Phe Phe Glu Pro Gly	
680	685	690
Leu His Cys Trp Ile Thr Gly Trp Gly	Ala Leu Arg Glu Gly Gly	
695	700	705
Pro Ile Ser Asn Ala Leu Gln Lys Val	Asp Val Gln Leu Ile Pro	
710	715	720
Gln Asp Leu Cys Ser Glu Ala Tyr Arg	Tyr Gln Val Thr Pro Arg	
725	730	735
Met Leu Cys Ala Gly Tyr Arg Lys Gly	Lys Lys Asp Ala Cys Gln	
740	745	750
Gly Asp Ser Gly Gly Pro Leu Val Cys	Lys Ala Leu Ser Gly Arg	
755	760	765
Trp Phe Leu Ala Gly Leu Val Ser Trp	Gly Leu Gly Cys Gly Arg	
770	775	780
Pro Asn Tyr Phe Gly Val Tyr Thr Arg	Ile Thr Gly Val Ile Ser	
785	790	795
Trp Ile Gln Gln Val Val Thr		
800		

<210> 170  
 <211> 1327  
 <212> DNA  
 <213> Homo sapiens

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 caccatcaac ttcacctccc agatctccct caccggggccc ggtgtgcggg 150  
 tgcactatgg cttgtacaac cagtcggacc cctgccctgg agagttcctc 200  
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 ccccaacggc ctggatgaga gaaactgcgt ttgcagagcc acattccagt 300  
 gcaaagagga cagcacatgc atctcactgc ccaaggtctg tgatgggcag 350  
 cctgattgtc tcaacggcag cgatgaagag cagtgccagg aaggggtgcc 400  
 atgtgggaca ttcaccttcc agtgtgagga ccggagctgc gtgaagaagc 450  
 ccaacccgca gtgtgatggg cggcccgact gcagggacgg ctcgatgag 500  
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gaccgtgttc ctgggcaagg tgtggcagaa ctcgcgctgg cctggagagg 750  
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ggtcagctgg ggctgggct gtggccggcc taactacttc ggcgtctaca 1200  
cccgcatcac aggtgtgatc agctggatcc agcaagtggg gacctgagga 1250  
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<210> 171

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

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<210> 172

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 172

taatccagca gtgcaggccg gg 22

<210> 173

<211> 50

<212> DNA



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 173

atggcctcca cgggtgctgtg gaccgtgttc ctgggcaagg tgtggcagaa 50

<210> 174

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 174

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<210> 175

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 175

aggcaggac acagagtcca ttcac 25

<210> 176

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 176

agtatgattt gccgtgcacc cagggccagt ggacgatcca gaacaggagg 50

<210> 177

<211> 1510

<212> DNA

<213> Homo sapiens

<400> 177

ggacgagggc agatctcggt ctggggcaag ccgttgacac tcgtccctg 50

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ctccagtccc ccagcccctg gccgagagaa gggctcttacc ggccgggatt 150

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agcatgaagg atgctacctc tccgtcggcc acagccagcc cttagaagac 450  
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caattgcata tggaacaatc acagaggtgg taaaatgtga gcatgagcga 1050  
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aataaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500  
aaaaaaaaaa 1510

<210> 178

<211> 354

<212> PRT

<213> Homo sapiens

<400> 178

Met	Ser	Asn	Ser	Val	Pro	Leu	Leu	Cys	Phe	Trp	Ser	Leu	Cys	Tyr	
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Cys	Phe	Ala	Ala	Gly	Ser	Pro	Val	Pro	Phe	Gly	Pro	Glu	Gly	Arg	
				20					25					30	
Leu	Glu	Asp	Lys	Leu	His	Lys	Pro	Lys	Ala	Thr	Gln	Thr	Glu	Val	
				35					40					45	
Lys	Pro	Ser	Val	Arg	Phe	Asn	Leu	Arg	Thr	Ser	Lys	Asp	Pro	Glu	
				50					55					60	
His	Glu	Gly	Cys	Tyr	Leu	Ser	Val	Gly	His	Ser	Gln	Pro	Leu	Glu	
				65					70					75	
Asp	Cys	Ser	Phe	Asn	Met	Thr	Ala	Lys	Thr	Phe	Phe	Ile	Ile	His	
				80					85					90	
Gly	Trp	Thr	Met	Ser	Gly	Ile	Phe	Glu	Asn	Trp	Leu	His	Lys	Leu	
				95					100					105	
Val	Ser	Ala	Leu	His	Thr	Arg	Glu	Lys	Asp	Ala	Asn	Val	Val	Val	
				110					115					120	
Val	Asp	Trp	Leu	Pro	Leu	Ala	His	Gln	Leu	Tyr	Thr	Asp	Ala	Val	
				125					130					135	
Asn	Asn	Thr	Arg	Val	Val	Gly	His	Ser	Ile	Ala	Arg	Met	Leu	Asp	
				140					145					150	
Trp	Leu	Gln	Glu	Lys	Asp	Asp	Phe	Ser	Leu	Gly	Asn	Val	His	Leu	
				155					160					165	
Ile	Gly	Tyr	Ser	Leu	Gly	Ala	His	Val	Ala	Gly	Tyr	Ala	Gly	Asn	
				170					175					180	
Phe	Val	Lys	Gly	Thr	Val	Gly	Arg	Ile	Thr	Gly	Leu	Asp	Pro	Ala	
				185					190					195	
Gly	Pro	Met	Phe	Glu	Gly	Ala	Asp	Ile	His	Lys	Arg	Leu	Ser	Pro	
				200					205					210	
Asp	Asp	Ala	Asp	Phe	Val	Asp	Val	Leu	His	Thr	Tyr	Thr	Arg	Ser	
				215					220					225	
Phe	Gly	Leu	Ser	Ile	Gly	Ile	Gln	Met	Pro	Val	Gly	His	Ile	Asp	
				230					235					240	
Ile	Tyr	Pro	Asn	Gly	Gly	Asp	Phe	Gln	Pro	Gly	Cys	Gly	Leu	Asn	
				245					250					255	
Asp	Val	Leu	Gly	Ser	Ile	Ala	Tyr	Gly	Thr	Ile	Thr	Glu	Val	Val	
				260					265					270	
Lys	Cys	Glu	His	Glu	Arg	Ala	Val	His	Leu	Phe	Val	Asp	Ser	Leu	
				275					280					285	

Val	Asn	Gln	Asp	Lys	Pro	Ser	Phe	Ala	Phe	Gln	Cys	Thr	Asp	Ser
				290					295					300
Asn	Arg	Phe	Lys	Lys	Gly	Ile	Cys	Leu	Ser	Cys	Arg	Lys	Asn	Arg
				305					310					315
Cys	Asn	Ser	Ile	Gly	Tyr	Asn	Ala	Lys	Lys	Met	Arg	Asn	Lys	Arg
				320					325					330
Asn	Ser	Lys	Met	Tyr	Leu	Lys	Thr	Arg	Ala	Gly	Met	Pro	Phe	Arg
				335					340					345
Gly	Asn	Leu	Gln	Ser	Leu	Glu	Cys	Pro						
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<210> 179

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 179

gtgagcatga gcgagccgtc cac 23

<210> 180

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 180

gctattacaa cggttcttgc ggcagc 26

<210> 181

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 181

ttgactctct ggtgaatcag gacaagccga gttttgcctt ccag 44

<210> 182

<211> 3240

<212> DNA

<213> Homo sapiens

<400> 182

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acgcgctgga ggagtggagc agcaccggc cggccctggg ggctgacagt 150  
cggcaaagt tggcccgaag aggaagtggc ctcaaacc cggcaggtggc 200  
gaccaggcca gaccaggggc gctcgtgcc tgcgggcggg ctgtaggcga 250  
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<210> 183

<211> 713

<212> PRT

<213> Homo sapiens

<400> 183

Met	Leu	Leu	Ala	Thr	Leu	Leu	Leu	Leu	Leu	Gly	Gly	Ala	Leu	1	5	10	15
Ala	His	Pro	Asp	Arg	Ile	Ile	Phe	Pro	Asn	His	Ala	Cys	Glu	Asp	20	25	30
Pro	Pro	Ala	Val	Leu	Leu	Glu	Val	Gln	Gly	Thr	Leu	Gln	Arg	Pro	35	40	45
Leu	Val	Arg	Asp	Ser	Arg	Thr	Ser	Pro	Ala	Asn	Cys	Thr	Trp	Leu	50	55	60
Ile	Leu	Gly	Ser	Lys	Glu	Gln	Thr	Val	Thr	Ile	Arg	Phe	Gln	Lys	65	70	75
Leu	His	Leu	Ala	Cys	Gly	Ser	Glu	Arg	Leu	Thr	Leu	Arg	Ser	Pro	80	85	90
Leu	Gln	Pro	Leu	Ile	Ser	Leu	Cys	Glu	Ala	Pro	Pro	Ser	Pro	Leu	95	100	105
Gln	Leu	Pro	Gly	Gly	Asn	Val	Thr	Ile	Thr	Tyr	Ser	Tyr	Ala	Gly	110	115	120
Ala	Arg	Ala	Pro	Met	Gly	Gln	Gly	Phe	Leu	Leu	Ser	Tyr	Ser	Gln	125	130	135
Asp	Trp	Leu	Met	Cys	Leu	Gln	Glu	Glu	Phe	Gln	Cys	Leu	Asn	His	140	145	150
Arg	Cys	Val	Ser	Ala	Val	Gln	Arg	Cys	Asp	Gly	Val	Asp	Ala	Cys	155	160	165
Gly	Asp	Gly	Ser	Asp	Glu	Ala	Gly	Cys	Ser	Ser	Asp	Pro	Phe	Pro	170	175	180
Gly	Leu	Thr	Pro	Arg	Pro	Val	Pro	Ser	Leu	Pro	Cys	Asn	Val	Thr			

185	190	195
Leu Glu Asp Phe Tyr Gly Val Phe Ser	Ser Pro Gly Tyr Thr His	
200	205	210
Leu Ala Ser Val Ser His Pro Gln Ser	Cys His Trp Leu Leu Asp	
215	220	225
Pro His Asp Gly Arg Arg Leu Ala Val	Arg Phe Thr Ala Leu Asp	
230	235	240
Leu Gly Phe Gly Asp Ala Val His Val	Tyr Asp Gly Pro Gly Pro	
245	250	255
Pro Glu Ser Ser Arg Leu Leu Arg Ser	Leu Thr His Phe Ser Asn	
260	265	270
Gly Lys Ala Val Thr Val Glu Thr Leu	Ser Gly Gln Ala Val Val	
275	280	285
Ser Tyr His Thr Val Ala Trp Ser Asn	Gly Arg Gly Phe Asn Ala	
290	295	300
Thr Tyr His Val Arg Gly Tyr Cys Leu	Pro Trp Asp Arg Pro Cys	
305	310	315
Gly Leu Gly Ser Gly Leu Gly Ala Gly	Glu Gly Leu Gly Glu Arg	
320	325	330
Cys Tyr Ser Glu Ala Gln Arg Cys Asp	Gly Ser Trp Asp Cys Ala	
335	340	345
Asp Gly Thr Asp Glu Glu Asp Cys Pro	Gly Cys Pro Pro Gly His	
350	355	360
Phe Pro Cys Gly Ala Ala Gly Thr Ser	Gly Ala Thr Ala Cys Tyr	
365	370	375
Leu Pro Ala Asp Arg Cys Asn Tyr Gln	Thr Phe Cys Ala Asp Gly	
380	385	390
Ala Asp Glu Arg Arg Cys Arg His Cys	Gln Pro Gly Asn Phe Arg	
395	400	405
Cys Arg Asp Glu Lys Cys Val Tyr Glu	Thr Trp Val Cys Asp Gly	
410	415	420
Gln Pro Asp Cys Ala Asp Gly Ser Asp	Glu Trp Asp Cys Ser Tyr	
425	430	435
Val Leu Pro Arg Lys Val Ile Thr Ala	Ala Val Ile Gly Ser Leu	
440	445	450
Val Cys Gly Leu Leu Leu Val Ile Ala	Leu Gly Cys Thr Cys Lys	
455	460	465
Leu Tyr Ala Ile Arg Thr Gln Glu Tyr	Ser Ile Phe Ala Pro Leu	



470	475	480
Ser Arg Met Glu Ala Glu Ile Val Gln	Gln Gln Ala Pro Pro Ser	
485	490	495
Tyr Gly Gln Leu Ile Ala Gln Gly Ala	Ile Pro Pro Val Glu Asp	
500	505	510
Phe Pro Thr Glu Asn Pro Asn Asp Asn	Ser Val Leu Gly Asn Leu	
515	520	525
Arg Ser Leu Leu Gln Ile Leu Arg Gln	Asp Met Thr Pro Gly Gly	
530	535	540
Gly Pro Gly Ala Arg Arg Arg Gln Arg	Gly Arg Leu Met Arg Arg	
545	550	555
Leu Val Arg Arg Leu Arg Arg Trp Gly	Leu Leu Pro Arg Thr Asn	
560	565	570
Thr Pro Ala Arg Ala Ser Glu Ala Arg	Ser Gln Val Thr Pro Ser	
575	580	585
Ala Ala Pro Leu Glu Ala Leu Asp Gly	Gly Thr Gly Pro Ala Arg	
590	595	600
Glu Gly Gly Ala Val Gly Gly Gln Asp	Gly Glu Gln Ala Pro Pro	
605	610	615
Leu Pro Ile Lys Ala Pro Leu Pro Ser	Ala Ser Thr Ser Pro Ala	
620	625	630
Pro Thr Thr Val Pro Glu Ala Pro Gly	Pro Leu Pro Ser Leu Pro	
635	640	645
Leu Glu Pro Ser Leu Leu Ser Gly Val	Val Gln Ala Leu Arg Gly	
650	655	660
Arg Leu Leu Pro Ser Leu Gly Pro Pro	Gly Pro Thr Arg Ser Pro	
665	670	675
Pro Gly Pro His Thr Ala Val Leu Ala	Leu Glu Asp Glu Asp Asp	
680	685	690
Val Leu Leu Val Pro Leu Ala Glu Pro	Gly Val Trp Val Ala Glu	
695	700	705
Ala Glu Asp Glu Pro Leu Leu Thr		
710		

<210> 184

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 184  
ggctgtcact gtggagacac 20

<210> 185  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 185  
gcaaggtcat tacagctg 18

<210> 186  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 186  
agaacatagg agcagtccca ctc 23

<210> 187  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 187  
tgcctgctgc tgcacaatct cag 23

<210> 188  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 188  
ggctattgct tgccttggga cagaccctgt ggcttaggct ctggc 45

<210> 189  
<211> 663  
<212> DNA  
<213> Homo sapiens

<400> 189  
cgagctgggc gagaagtagg ggagggcggt gctccgccgc ggtggcggtt 50  
gctatcgctt cgcagaacct actcaggcag ccagctgaga agagttgagg 100

gaaagtgctg ctgctgggtc tgcagacgcg atggataacg tgcagccgaa 150  
 aataaaacat cgccccttct gcttcagtgt gaaaggccac gtgaagatgc 200  
 tgccgctggc actaactgtg acatctatga ccttttttat catcgacaaa 250  
 gccctgaac catatattgt tatcactgga tttgaagtca ccgttatctt 300  
 atttttcata cttttatatg tactcagact tgatcgatta atgaagtggg 350  
 tattttggcc tttgcttgat attatcaact cactggtaac aacagtattc 400  
 atgctcatcg tatctgtgtt ggccactgata ccagaaacca caacattgac 450  
 agttgggtgga ggggtgtttg cacttgtgac agcagtatgc tgtcttgccg 500  
 acggggccct tatttaccgg aagcttctgt tcaatcccag cggtccttac 550  
 cagaaaaagc ctgtgcatga aaaaaaagaa gttttgtaat tttatattac 600  
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 aaaaaaaaaa aaa 663

<210> 190

<211> 152

<212> PRT

<213> Homo sapiens

<400> 190

Met	Asp	Asn	Val	Gln	Pro	Lys	Ile	Lys	His	Arg	Pro	Phe	Cys	Phe
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Ser	Val	Lys	Gly	His	Val	Lys	Met	Leu	Arg	Leu	Ala	Leu	Thr	Val
			20						25					30

Thr	Ser	Met	Thr	Phe	Phe	Ile	Ile	Ala	Gln	Ala	Pro	Glu	Pro	Tyr
				35					40					45

Ile	Val	Ile	Thr	Gly	Phe	Glu	Val	Thr	Val	Ile	Leu	Phe	Phe	Ile
				50					55					60

Leu	Leu	Tyr	Val	Leu	Arg	Leu	Asp	Arg	Leu	Met	Lys	Trp	Leu	Phe
				65					70					75

Trp	Pro	Leu	Leu	Asp	Ile	Ile	Asn	Ser	Leu	Val	Thr	Thr	Val	Phe
				80					85					90

Met	Leu	Ile	Val	Ser	Val	Leu	Ala	Leu	Ile	Pro	Glu	Thr	Thr	Thr
				95					100					105

Leu	Thr	Val	Gly	Gly	Gly	Val	Phe	Ala	Leu	Val	Thr	Ala	Val	Cys
				110					115					120

Cys	Leu	Ala	Asp	Gly	Ala	Leu	Ile	Tyr	Arg	Lys	Leu	Leu	Phe	Asn
				125					130					135

Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu  
140 145 150

Val Leu

<210> 191  
<211> 495  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 78, 212, 234, 487  
<223> unknown base

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ctgctgctgg gtctgcagac gcgatggata acgtgcagcc gaaaataaaa 150  
catcgcccct tctgcttcag tgtgaaaggc cacgtgaaga tgctgcggct 200  
ggcactaact gngacatcta tgacctttt tatnatcgca caagcccctg 250  
aaccatatat tgttatcact ggatttgaag tcaccgttat cttatttttc 300  
atacttttat atgtactcag acttgatcga ttaatgaagt ggttattttg 350  
gcctttgctt gatattatca actcactggg aacaacagta ttcattgctca 400  
tcgtatctgt gttggcactg ataccagaaa ccacaacatt gacagttggt 450  
ggaggggtgt ttgcaottgt gacagcagta tgctgtnttg ccgac 495

<210> 192  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 192  
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<210> 193  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 193  
cctccaccaa ctgtcaatgt tgtgg 25

<210> 194

<211> 40

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 194

aaagtgtgc tgctgggtct gcagacgcga tggataacgt 40

<210> 195

<211> 1879

<212> DNA

<213> Homo sapien

<400> 195

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ggaccggcta ggctgggcgc gcccccggg ccccgccgtg ggcatgggcg 100  
cactggcccg ggcgtgctg ctgcctctgc tggcccagtg gtcctgcgc 150  
gcgcccccg agctggcccc cgcgcccttc acgctgcccc tccgggtggc 200  
cgcggccacg aaccgcgtag ttgcgcccac cccgggaccc gggaccctg 250  
ccgagcgcca cgccgacggc ttggcgctcg ccctggagcc tgccctggcg 300  
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ggaacccccg actcctacat agacacgtac tttgacacag agaggtctag 500  
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gtggaagctg tggcccgcgc atctctgatt ccagaattct ctgatgggtt 1100  
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atgcgctggg gatcggtgcc acgggtgatgg agggcttcta cgtcatcttc 1350  
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tagccagcaa ctgtgtcccc gctcagtctt tgagcgagcc cattttgtgg 1500  
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acatttccag ggcagcagcc gggatcgatg gtggcgcttt ctctgtgcc 1750  
caccctctt caatctctgt tctgtccca gatgccttct agattcactg 1800  
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aaataattaa aaaaaaaact tcattctaa 1879

<210> 196

<211> 518

<212> PRT.

<213> Homo sapien

<400> 196

Met	Gly	Ala	Leu	Ala	Arg	Ala	Leu	Leu	Leu	Pro	Leu	Leu	Ala	Gln
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Trp	Leu	Leu	Arg	Ala	Ala	Pro	Glu	Leu	Ala	Pro	Ala	Pro	Phe	Thr
			20						25					30

Leu	Pro	Leu	Arg	Val	Ala	Ala	Ala	Thr	Asn	Arg	Val	Val	Ala	Pro
			35						40					45

Thr	Pro	Gly	Pro	Gly	Thr	Pro	Ala	Glu	Arg	His	Ala	Asp	Gly	Leu
			50						55					60

Ala	Leu	Ala	Leu	Glu	Pro	Ala	Leu	Ala	Ser	Pro	Ala	Gly	Ala	Ala			
				65					70					75			
Asn	Phe	Leu	Ala	Met	Val	Asp	Asn	Leu	Gln	Gly	Asp	Ser	Gly	Arg			
				80					85					90			
Gly	Tyr	Tyr	Leu	Glu	Met	Leu	Ile	Gly	Thr	Pro	Pro	Gln	Lys	Leu			
				95					100					105			
Gln	Ile	Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Ala	Gly			
				110					115					120			
Thr	Pro	His	Ser	Tyr	Ile	Asp	Thr	Tyr	Phe	Asp	Thr	Glu	Arg	Ser			
				125					130					135			
Ser	Thr	Tyr	Arg	Ser	Lys	Gly	Phe	Asp	Val	Thr	Val	Lys	Tyr	Thr			
				140					145					150			
Gln	Gly	Ser	Trp	Thr	Gly	Phe	Val	Gly	Glu	Asp	Leu	Val	Thr	Ile			
				155					160					165			
Pro	Lys	Gly	Phe	Asn	Thr	Ser	Phe	Leu	Val	Asn	Ile	Ala	Thr	Ile			
				170					175					180			
Phe	Glu	Ser	Glu	Asn	Phe	Phe	Leu	Pro	Gly	Ile	Lys	Trp	Asn	Gly			
				185					190					195			
Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Thr	Leu	Ala	Lys	Pro	Ser	Ser	Ser			
				200					205					210			
Leu	Glu	Thr	Phe	Phe	Asp	Ser	Leu	Val	Thr	Gln	Ala	Asn	Ile	Pro			
				215					220					225			
Asn	Val	Phe	Ser	Met	Gln	Met	Cys	Gly	Ala	Gly	Leu	Pro	Val	Ala			
				230					235					240			
Gly	Ser	Gly	Thr	Asn	Gly	Gly	Ser	Leu	Val	Leu	Gly	Gly	Ile	Glu			
				245					250					255			
Pro	Ser	Leu	Tyr	Lys	Gly	Asp	Ile	Trp	Tyr	Thr	Pro	Ile	Lys	Glu			
				260					265					270			
Glu	Trp	Tyr	Tyr	Gln	Ile	Glu	Ile	Leu	Lys	Leu	Glu	Ile	Gly	Gly			
				275					280					285			
Gln	Ser	Leu	Asn	Leu	Asp	Cys	Arg	Glu	Tyr	Asn	Ala	Asp	Lys	Ala			
				290					295					300			
Ile	Val	Asp	Ser	Gly	Thr	Thr	Leu	Leu	Arg	Leu	Pro	Gln	Lys	Val			
				305					310					315			
Phe	Asp	Ala	Val	Val	Glu	Ala	Val	Ala	Arg	Ala	Ser	Leu	Ile	Pro			
				320					325					330			
Glu	Phe	Ser	Asp	Gly	Phe	Trp	Thr	Gly	Ser	Gln	Leu	Ala	Cys	Trp			
				335					340					345			

Thr Asn Ser Glu	Thr Pro Trp Ser Tyr	Phe Pro Lys Ile Ser	Ile
350		355	360
Tyr Leu Arg Asp	Glu Asn Ser Ser Arg	Ser Phe Arg Ile Thr	Ile
365		370	375
Leu Pro Gln Leu	Tyr Ile Gln Pro Met	Met Gly Ala Gly Leu	Asn
380		385	390
Tyr Glu Cys Tyr	Arg Phe Gly Ile Ser	Pro Ser Thr Asn Ala	Leu
395		400	405
Val Ile Gly Ala	Thr Val Met Glu Gly	Phe Tyr Val Ile Phe	Asp
410		415	420
Arg Ala Gln Lys	Arg Val Gly Phe Ala	Ala Ser Pro Cys Ala	Glu
425		430	435
Ile Ala Gly Ala	Ala Val Ser Glu Ile	Ser Gly Pro Phe Ser	Thr
440		445	450
Glu Asp Val Ala	Ser Asn Cys Val Pro	Ala Gln Ser Leu Ser	Glu
455		460	465
Pro Ile Leu Trp	Ile Val Ser Tyr Ala	Leu Met Ser Val Cys	Gly
470		475	480
Ala Ile Leu Leu	Val Leu Ile Val Leu	Leu Leu Leu Pro Phe	Arg
485		490	495
Cys Gln Arg Arg	Pro Arg Asp Pro Glu	Val Val Asn Asp Glu	Ser
500		505	510
Ser Leu Val Arg	His Arg Trp Lys		
515			

<210> 197

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 197

cgcagaagct acagattctc g 21

<210> 198

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 198

ggaaattgga ggccaaagc 19



<210> 199  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 199  
ggatgtagcc agcaactgtg 20

<210> 200  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 200  
gccttggctc gttctcttc 19

<210> 201  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 201  
ggtcctgtgc ctggatgg 18

<210> 202  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 202  
gacaagacta cctccgttgg tc 22

<210> 203  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 203  
tgatgcacag ttcagcacct gttg 24

<210> 204

<211> 47  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 204  
cgctccaagg gctttgacgt cacagtgaag tacacacaag gaagctg 47

<210> 205  
<211> 1939  
<212> DNA  
<213> Homo sapiens

<400> 205  
cgctccgcc ttcggaggct gacgcgccg ggcgccgttc caggcctgtg 50  
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gggcgggagc cgggaggcgc ggccggcatg gaggcgctgc tgctgggcgc 150  
ggggttgctg ctgggcgctt acgtgcttgt ctactacaac ctggtgaagg 200  
ccccgccgtg cggcggcatg ggcaacctgc ggggccgcac ggccgtggtc 250  
acgggcgcca acagcggcat cggaaagatg acggcgctgg agctggcgcg 300  
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cagggcaggg cagctggtat cgagggtccc catgggagta aggggacgcc 1850  
ttccgggcgg atgcagggtt ggggtcatct gtatctgaag cccctcgga 1900  
taaagcgcgt tgaccgcaa aaaaaaaaaa aaaaaaaaaa 1939

<210> 206

<211> 377

<212> PRT

<213> Homo sapiens

<400> 206

Met	Glu	Ala	Leu	Leu	Leu	Gly	Ala	Gly	Leu	Leu	Leu	Gly	Ala	Tyr
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Val	Leu	Val	Tyr	Tyr	Asn	Leu	Val	Lys	Ala	Pro	Pro	Cys	Gly	Gly
				20					25					30

Met	Gly	Asn	Leu	Arg	Gly	Arg	Thr	Ala	Val	Val	Thr	Gly	Ala	Asn
				35					40					45

Ser	Gly	Ile	Gly	Lys	Met	Thr	Ala	Leu	Glu	Leu	Ala	Arg	Arg	Gly
				50					55					60

Ala	Arg	Val	Val	Leu	Ala	Cys	Arg	Ser	Gln	Glu	Arg	Gly	Glu	Ala
				65					70					75

Ala Ala Phe Asp Leu Arg Gln Glu Ser Gly Asn Asn Glu Val Ile	80	85	90
Phe Met Ala Leu Asp Leu Ala Ser Leu Ala Ser Val Arg Ala Phe	95	100	105
Ala Thr Ala Phe Leu Ser Ser Glu Pro Arg Leu Asp Ile Leu Ile	110	115	120
His Asn Ala Gly Ile Ser Ser Cys Gly Arg Thr Arg Glu Ala Phe	125	130	135
Asn Leu Leu Leu Arg Val Asn His Ile Gly Pro Phe Leu Leu Thr	140	145	150
His Leu Leu Leu Pro Cys Leu Lys Ala Cys Ala Pro Ser Arg Val	155	160	165
Val Val Val Ala Ser Ala Ala His Cys Arg Gly Arg Leu Asp Phe	170	175	180
Lys Arg Leu Asp Arg Pro Val Val Gly Trp Arg Gln Glu Leu Arg	185	190	195
Ala Tyr Ala Asp Thr Lys Leu Ala Asn Val Leu Phe Ala Arg Glu	200	205	210
Leu Ala Asn Gln Leu Glu Ala Thr Gly Val Thr Cys Tyr Ala Ala	215	220	225
His Pro Gly Pro Val Asn Ser Glu Leu Phe Leu Arg His Val Pro	230	235	240
Gly Trp Leu Arg Pro Leu Leu Arg Pro Leu Ala Trp Leu Val Leu	245	250	255
Arg Ala Pro Arg Gly Gly Ala Gln Thr Pro Leu Tyr Cys Ala Leu	260	265	270
Gln Glu Gly Ile Glu Pro Leu Ser Gly Arg Tyr Phe Ala Asn Cys	275	280	285
His Val Glu Glu Val Pro Pro Ala Ala Arg Asp Asp Arg Ala Ala	290	295	300
His Arg Leu Trp Glu Ala Ser Lys Arg Leu Ala Gly Leu Gly Pro	305	310	315
Gly Glu Asp Ala Glu Pro Asp Glu Asp Pro Gln Ser Glu Asp Ser	320	325	330
Glu Ala Pro Ser Ser Leu Ser Thr Pro His Pro Glu Glu Pro Thr	335	340	345
Val Ser Gln Pro Tyr Pro Ser Pro Gln Ser Ser Pro Asp Leu Ser	350	355	360

Lys Met Thr His Arg Ile Gln Ala Lys Val Glu Pro Glu Ile Gln  
365 370 375

Leu Ser

<210> 207  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 207  
cttcatggcc ttggacttgg ccag 24

<210> 208  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 208  
acgccagtgg cctcaagctg gttg 24

<210> 209  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 209  
ctttctgagc tctgagccac gggttgacat cctcatccac aatgc 45

<210> 210  
<211> 3716  
<212> DNA  
<213> Homo sapiens

<400> 210  
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acccccagga ccagctgttc cagggccctg gccctgccag gatgagctgc 150  
caagcctcag gccagccacc tcccaccatc cgctgggttg tgaatgggca 200  
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<210> 211  
 <211> 985  
 <212> PRT  
 <213> Homo sapiens

<400> 211

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			20						25					30
Cys	Gln	Ala	Ser	Gly	Gln	Pro	Pro	Pro	Thr	Ile	Arg	Trp	Leu	Leu
			35						40					45
Asn	Gly	Gln	Pro	Leu	Ser	Met	Val	Pro	Pro	Asp	Pro	His	His	Leu
			50						55					60
Leu	Pro	Asp	Gly	Thr	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Ala	Arg	Gly
			65						70					75
His	Ala	His	Asp	Gly	Gln	Ala	Leu	Ser	Thr	Asp	Leu	Gly	Val	Tyr
			80						85					90
Thr	Cys	Glu	Ala	Ser	Asn	Arg	Leu	Gly	Thr	Ala	Val	Ser	Arg	Gly
			95						100					105
Ala	Arg	Leu	Ser	Val	Ala	Val	Leu	Arg	Glu	Asp	Phe	Gln	Ile	Gln
			110						115					120
Pro	Arg	Asp	Met	Val	Ala	Val	Val	Gly	Glu	Gln	Phe	Thr	Leu	Glu
			125						130					135



Cys Gly Pro Pro Trp Gly His Pro Glu Pro Thr Val Ser Trp Trp	140	145	150
Lys Asp Gly Lys Pro Leu Ala Leu Gln Pro Gly Arg His Thr Val	155	160	165
Ser Gly Gly Ser Leu Leu Met Ala Arg Ala Glu Lys Ser Asp Glu	170	175	180
Gly Thr Tyr Met Cys Val Ala Thr Asn Ser Ala Gly His Arg Glu	185	190	195
Ser Arg Ala Ala Arg Val Ser Ile Gln Glu Pro Gln Asp Tyr Thr	200	205	210
Glu Pro Val Glu Leu Leu Ala Val Arg Ile Gln Leu Glu Asn Val	215	220	225
Thr Leu Leu Asn Pro Asp Pro Ala Glu Gly Pro Lys Pro Arg Pro	230	235	240
Ala Val Trp Leu Ser Trp Lys Val Ser Gly Pro Ala Ala Pro Ala	245	250	255
Gln Ser Tyr Thr Ala Leu Phe Arg Thr Gln Thr Ala Pro Gly Gly	260	265	270
Gln Gly Ala Pro Trp Ala Glu Glu Leu Leu Ala Gly Trp Gln Ser	275	280	285
Ala Glu Leu Gly Gly Leu His Trp Gly Gln Asp Tyr Glu Phe Lys	290	295	300
Val Arg Pro Ser Ser Gly Arg Ala Arg Gly Pro Asp Ser Asn Val	305	310	315
Leu Leu Leu Arg Leu Pro Glu Lys Val Pro Ser Ala Pro Pro Gln	320	325	330
Glu Val Thr Leu Lys Pro Gly Asn Gly Thr Val Phe Val Ser Trp	335	340	345
Val Pro Pro Pro Ala Glu Asn His Asn Gly Ile Ile Arg Gly Tyr	350	355	360
Gln Val Trp Ser Leu Gly Asn Thr Ser Leu Pro Pro Ala Asn Trp	365	370	375
Thr Val Val Gly Glu Gln Thr Gln Leu Glu Ile Ala Thr His Met	380	385	390
Pro Gly Ser Tyr Cys Val Gln Val Ala Ala Val Thr Gly Ala Gly	395	400	405
Ala Gly Glu Pro Ser Arg Pro Val Cys Leu Leu Leu Glu Gln Ala	410	415	420

Met Glu Arg Ala Thr Gln Glu Pro Ser Glu His Gly Pro Trp Thr	425	430	435
Leu Glu Gln Leu Arg Ala Thr Leu Lys Arg Pro Glu Val Ile Ala	440	445	450
Thr Cys Gly Val Ala Leu Trp Leu Leu Leu Leu Gly Thr Ala Val	455	460	465
Cys Ile His Arg Arg Arg Arg Ala Arg Val His Leu Gly Pro Gly	470	475	480
Leu Tyr Arg Tyr Thr Ser Glu Asp Ala Ile Leu Lys His Arg Met	485	490	495
Asp His Ser Asp Ser Gln Trp Leu Ala Asp Thr Trp Arg Ser Thr	500	505	510
Ser Gly Ser Arg Asp Leu Ser Ser Ser Ser Ser Leu Ser Ser Arg	515	520	525
Leu Gly Ala Asp Ala Arg Asp Pro Leu Asp Cys Arg Arg Ser Leu	530	535	540
Leu Ser Trp Asp Ser Arg Ser Pro Gly Val Pro Leu Leu Pro Asp	545	550	555
Thr Ser Thr Phe Tyr Gly Ser Leu Ile Ala Glu Leu Pro Ser Ser	560	565	570
Thr Pro Ala Arg Pro Ser Pro Gln Val Pro Ala Val Arg Arg Leu	575	580	585
Pro Pro Gln Leu Ala Gln Leu Ser Ser Pro Cys Ser Ser Ser Asp	590	595	600
Ser Leu Cys Ser Arg Arg Gly Leu Ser Ser Pro Arg Leu Ser Leu	605	610	615
Ala Pro Ala Glu Ala Trp Lys Ala Lys Lys Lys Gln Glu Leu Gln	620	625	630
His Ala Asn Ser Ser Pro Leu Leu Arg Gly Ser His Ser Leu Glu	635	640	645
Leu Arg Ala Cys Glu Leu Gly Asn Arg Gly Ser Lys Asn Leu Ser	650	655	660
Gln Ser Pro Gly Ala Val Pro Gln Ala Leu Val Ala Trp Arg Ala	665	670	675
Leu Gly Pro Lys Leu Leu Ser Ser Ser Asn Glu Leu Val Thr Arg	680	685	690
His Leu Pro Pro Ala Pro Leu Phe Pro His Glu Thr Pro Pro Thr	695	700	705

Gln Ser Gln Gln Thr Gln Pro Pro Val Ala Pro Gln Ala Pro Ser	710	715	720
Ser Ile Leu Leu Pro Ala Ala Pro Ile Pro Ile Leu Ser Pro Cys	725	730	735
Ser Pro Pro Ser Pro Gln Ala Ser Ser Leu Ser Gly Pro Ser Pro	740	745	750
Ala Ser Ser Arg Leu Ser Ser Ser Ser Leu Ser Ser Leu Gly Glu	755	760	765
Asp Gln Asp Ser Val Leu Thr Pro Glu Glu Val Ala Leu Cys Leu	770	775	780
Glu Leu Ser Glu Gly Glu Glu Thr Pro Arg Asn Ser Val Ser Pro	785	790	795
Met Pro Arg Ala Pro Ser Pro Pro Thr Thr Tyr Gly Tyr Ile Ser	800	805	810
Val Pro Thr Ala Ser Glu Phe Thr Asp Met Gly Arg Thr Gly Gly	815	820	825
Gly Val Gly Pro Lys Gly Gly Val Leu Leu Cys Pro Pro Arg Pro	830	835	840
Cys Leu Thr Pro Thr Pro Ser Glu Gly Ser Leu Ala Asn Gly Trp	845	850	855
Gly Ser Ala Ser Glu Asp Asn Ala Ala Ser Ala Arg Ala Ser Leu	860	865	870
Val Ser Ser Ser Asp Gly Ser Phe Leu Ala Asp Ala His Phe Ala	875	880	885
Arg Ala Leu Ala Val Ala Val Asp Ser Phe Gly Phe Gly Leu Glu	890	895	900
Pro Arg Glu Ala Asp Cys Val Phe Ile Asp Ala Ser Ser Pro Pro	905	910	915
Ser Pro Arg Asp Glu Ile Phe Leu Thr Pro Asn Leu Ser Leu Pro	920	925	930
Leu Trp Glu Trp Arg Pro Asp Trp Leu Glu Asp Met Glu Val Ser	935	940	945
His Thr Gln Arg Leu Gly Arg Gly Met Pro Pro Trp Pro Pro Asp	950	955	960
Ser Gln Ile Ser Ser Gln Arg Ser Gln Leu His Cys Arg Met Pro	965	970	975
Lys Ala Gly Ala Ser Pro Val Asp Tyr Ser	980	985	

<210> 212  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 212  
gaagggacct acatgtgtgt ggcc 24

<210> 213  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 213  
actgaccttc cagctgagcc acac 24

<210> 214  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 214  
aggactacac ggagcctgtg gagcttctgg ctgtgcgaat tcagctggaa 50

<210> 215  
<211> 2749  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1869, 1887  
<223> unknown base

<400> 215  
ctccacgggt gtccagcgcc cagaatgcgg cttctggtcc tgctatgggg 50  
  
ttgcctgctg ctcccagggt atgaagccct ggagggccca gaggaatca 100  
  
gcgggttcga aggggacact gtgtccctgc agtgcaccta cagggaagag 150  
  
ctgagggacc accggaagta ctggtgcagg aagggtggga tcctcttctc 200  
  
tcgctgctct ggcaccatct atgcagaaga agaaggccag gagacaatga 250  
  
agggcagggt gtccatccgt gacagccgcc aggagctctc gtcattgtg 300

acctgtgga acctaccct gcaagacgt ggggagtact ggtgtgggt 350  
cgaaaaacgg ggccccgatg agtctttact gatctctctg ttcgtcttcc 400  
caggaccctg ctgtctctcc tccccttctc ccaccttcca gcctctggct 450  
acaacacgcc tgcagcccaa ggcaaaagct cagcaaacc agccccagg 500  
attgacttct cctgggctct acccggcagc caccacagcc aagcagggga 550  
agacaggggc tgaggcccct ccattgccag ggacttccca gtacgggcac 600  
gaaaggactt ctcatgacac aggaacctct cctcaccag cgacctctcc 650  
tcctgcaggg agtccccgcc ccccatgca gctggactcc acctcagcag 700  
aggacaccag tccagctctc agcagtggca gctctaagcc cagggtgtcc 750  
atcccgatgg tccgcatact ggccccagtc ctggtgctgc tgagccttct 800  
gtcagccgca ggccctgatcg ccttctgcag ccacctgctc ctgtggagaa 850  
aggaagctca acaggccacg gagacacaga ggaacgagaa gttctggctc 900  
tcacgcttga ctgaggagga aaaggaagcc ccttcccagg cccctgaggg 950  
ggacgtgac tcgatgcctc cctccacac atctgaggag gagctgggct 1000  
tctcgaagtt tgtctcagcg tagggcagga ggccctctg gccaggccag 1050  
cagtgaagca gtatggctgg ctggatcagc acogattccc gaaagcttcc 1100  
cacctcagcc tcagagtcca gctgcccga ctccagggt cttcccacc 1150  
tcccaggct ctctcttgc atgttccagc ctgacctaga agcgtttgc 1200  
agccctggag ccagagcgg tggccttgc cttccggctg gagactggga 1250  
catccctgat aggttcacat ccctgggcag agtaccaggc tgctgaccct 1300  
cagcagggcc agacaaggct cagtggatct ggtctgagtt tcaatctgcc 1350  
aggaactcct gggcctcatg ccagtgctg gacctgcct tcctcccact 1400  
ccagacccca ccttgtcttc cctccctggc gtcctcagac ttagtccac 1450  
ggtctcctgc atcagctggg gatgaagagg agcatgctgg ggtgagactg 1500  
ggattctggc ttctctttga accacctgca tccagccctt caggaagcct 1550  
gtgaaaaacg tgattcctgg cccaccaag accacaaa accatctctg 1600  
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tgagtttgag ggccagtggg cctgatgaac gtcacaccc cttcagctta 1700  
gagctctcat ttgggctgtg acgtctccac ctgcccacat agatctgctc 1750

tgtctgcgac accagatcca cgtggggact cccctgaggc ctgctaagtc 1800  
 caggccttgg tcaggtcagg tgcacattgc aggataagcc caggaccggc 1850  
 acagaagtgg ttgcctttnc catttgccct ccctgggncca tgccttcttg 1900  
 cctttggaaa aaatgatgaa gaaaaccttg gctccttcct tgtctggaaa 1950  
 gggttacttg cctatgggtt ctgggtggcta gagagaaaag tagaaaacca 2000  
 gagtgcacgt aggtgtctaa cacagaggag agtaggaaca gggcggatac 2050  
 ctgaaggtga ctccgagtcc agccccctgg agaaggggtc gggggtggtg 2100  
 gtaaagtagc acaactacta ttttttttct ttttccatta ttattgtttt 2150  
 ttaagacaga atctcgtgct gctgcccagg ctggagtga gtggcacgat 2200  
 ctgcaaactc cgcctcctgg gttcaagtga ttcttctgcc tcagcctccc 2250  
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 cttttagtag agatgggggtt tcaccatggt ggccaggctg gtcttgaact 2350  
 cctgacctca aatgagcctc ctgcttcagt ctcccaaatt gccgggatta 2400  
 caggcatgag ccactgtgtc tggccctatt tcctttaaaa agtgaaatta 2450  
 agagttgttc agtatgcaaa acttggaag atggaggaga aaaagaaaag 2500  
 gaagaaaaaa atgtcaccca tagtctcacc agagactatc attatttcgt 2550  
 tttgtgttac ttccttcac tcttttcttc ttcacataat ttgccggtgt 2600  
 tctttttaca gagcaattat cttgtatata caactttgta tcttgccctt 2650  
 tccaccttat cgttccatca ctttattcca gcacttctct gtgttttaca 2700  
 gaccttttta taaataaaat gttcatcagc tgcataaaaa aaaaaaaaaa 2749

<210> 216

<211> 332

<212> PRT

<213> Homo sapiens

<400> 216

Met	Arg	Leu	Leu	Val	Leu	Leu	Trp	Gly	Cys	Leu	Leu	Leu	Pro	Gly
1				5				10					15	

Tyr	Glu	Ala	Leu	Glu	Gly	Pro	Glu	Glu	Ile	Ser	Gly	Phe	Glu	Gly
				20					25					30

Asp	Thr	Val	Ser	Leu	Gln	Cys	Thr	Tyr	Arg	Glu	Glu	Leu	Arg	Asp
				35					40					45

His Arg Lys Tyr Trp Cys Arg Lys Gly Gly Ile Leu Phe Ser Arg

50										55					60				
Cys	Ser	Gly	Thr	Ile	Tyr	Ala	Glu	Glu	Glu	Gly	Gln	Glu	Thr	Met					
				65										70					75
Lys	Gly	Arg	Val	Ser	Ile	Arg	Asp	Ser	Arg	Gln	Glu	Leu	Ser	Leu					
				80										85					90
Ile	Val	Thr	Leu	Trp	Asn	Leu	Thr	Leu	Gln	Asp	Ala	Gly	Glu	Tyr					
				95										100					105
Trp	Cys	Gly	Val	Glu	Lys	Arg	Gly	Pro	Asp	Glu	Ser	Leu	Leu	Ile					
				110										115					120
Ser	Leu	Phe	Val	Phe	Pro	Gly	Pro	Cys	Cys	Pro	Pro	Ser	Pro	Ser					
				125										130					135
Pro	Thr	Phe	Gln	Pro	Leu	Ala	Thr	Thr	Arg	Leu	Gln	Pro	Lys	Ala					
				140										145					150
Lys	Ala	Gln	Gln	Thr	Gln	Pro	Pro	Gly	Leu	Thr	Ser	Pro	Gly	Leu					
				155										160					165
Tyr	Pro	Ala	Ala	Thr	Thr	Ala	Lys	Gln	Gly	Lys	Thr	Gly	Ala	Glu					
				170										175					180
Ala	Pro	Pro	Leu	Pro	Gly	Thr	Ser	Gln	Tyr	Gly	His	Glu	Arg	Thr					
				185										190					195
Ser	Gln	Tyr	Thr	Gly	Thr	Ser	Pro	His	Pro	Ala	Thr	Ser	Pro	Pro					
				200										205					210
Ala	Gly	Ser	Ser	Arg	Pro	Pro	Met	Gln	Leu	Asp	Ser	Thr	Ser	Ala					
				215										220					225
Glu	Asp	Thr	Ser	Pro	Ala	Leu	Ser	Ser	Gly	Ser	Ser	Lys	Pro	Arg					
				230										235					240
Val	Ser	Ile	Pro	Met	Val	Arg	Ile	Leu	Ala	Pro	Val	Leu	Val	Leu					
				245										250					255
Leu	Ser	Leu	Leu	Ser	Ala	Ala	Gly	Leu	Ile	Ala	Phe	Cys	Ser	His					
				260										265					270
Leu	Leu	Leu	Trp	Arg	Lys	Glu	Ala	Gln	Gln	Ala	Thr	Glu	Thr	Gln					
				275										280					285
Arg	Asn	Glu	Lys	Phe	Trp	Leu	Ser	Arg	Leu	Thr	Ala	Glu	Glu	Lys					
				290										295					300
Glu	Ala	Pro	Ser	Gln	Ala	Pro	Glu	Gly	Asp	Val	Ile	Ser	Met	Pro					
				305										310					315
Pro	Leu	His	Thr	Ser	Glu	Glu	Glu	Leu	Gly	Phe	Ser	Lys	Phe	Val					
				320										325					330

Ser Ala

<210> 217  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 217  
ccctgcagtg cacctacagg gaag 24

<210> 218  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 218  
ctgtcttccc ctgcttggt gtgg 24

<210> 219  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 219  
ggtgcaggaa ggggtggatc ctcttctctc gctgctctgg ccacatc 47

<210> 220  
<211> 950  
<212> DNA  
<213> Homo sapiens

<400> 220  
ttgtgactaa aagctggcct agcaggccag ggagtgcagc tgcaggcgtg 50  
ggggtggcag gagccgcaga gccagagcag acagccgaga aacaggtgga 100  
cagtgtgaaa gaaccagtgg tctcgctctg ttgccagggc tagagtgtac 150  
tggcgtgata atagctcact gcagcctcag actcctggac ttgagaaatc 200  
ctcctgcctt agcctcctgc atatctggga ctccaggggt gcaactcaagc 250  
cctgtttctt ctcttctgt gagtggacca cggaggctgg tgagctgcct 300  
gtcatcccaa agctcagctc tgagccagag tgggtggtggc tccacctctg 350  
ccgccggcat agaagccagg agcagggctc tcagaaggcg gtggtgcccc 400



gctgggatca tgttggtggc cctgggtctgt ctgctcagct gcctgctacc 450  
 ctccagttag gccaaactct acggtcgttg tgaactggcc agagtgtac 500  
 atgacttcgg gctggacgga taccggggat acagcctggc tgactgggtc 550  
 tgccttgctt atttcacaag cggtttcaac gcagctgctt tggactacga 600  
 ggctgatggg agcaccaaca acgggatctt ccagatcaac agccggaggt 650  
 ggtgcagcaa cctcaccctg aacgtcccca acgtgtgccg gatgtactgc 700  
 tcagatttgt tgaatcctaa tctcaaggat accgttatct gtgccatgaa 750  
 gataacccaa gagcctcagg gtctgggtta ctgggaggcc tggaggcatc 800  
 actgccaggg aaaagacctc actgaatggg tggatggctg tgacttctag 850  
 gatggacgga accatgcaca gcaggctggg aaatgtggtt tggttcctga 900  
 cctaggcttg ggaagacaag ccagcgaata aaggatggtt gaacgtgaaa 950

<210> 221

<211> 146

<212> PRT

<213> Homo sapiens

<400> 221

Met	Leu	Leu	Ala	Leu	Val	Cys	Leu	Leu	Ser	Cys	Leu	Leu	Pro	Ser
1				5					10					15

Ser	Glu	Ala	Lys	Leu	Tyr	Gly	Arg	Cys	Glu	Leu	Ala	Arg	Val	Leu
				20					25					30

His	Asp	Phe	Gly	Leu	Asp	Gly	Tyr	Arg	Gly	Tyr	Ser	Leu	Ala	Asp
				35					40					45

Trp	Val	Cys	Leu	Ala	Tyr	Phe	Thr	Ser	Gly	Phe	Asn	Ala	Ala	Ala
				50					55					60

Leu	Asp	Tyr	Glu	Ala	Asp	Gly	Ser	Thr	Asn	Asn	Gly	Ile	Phe	Gln
				65					70					75

Ile	Asn	Ser	Arg	Arg	Trp	Cys	Ser	Asn	Leu	Thr	Pro	Asn	Val	Pro
				80					85					90

Asn	Val	Cys	Arg	Met	Tyr	Cys	Ser	Asp	Leu	Leu	Asn	Pro	Asn	Leu
				95					100					105

Lys	Asp	Thr	Val	Ile	Cys	Ala	Met	Lys	Ile	Thr	Gln	Glu	Pro	Gln
				110					115					120

Gly	Leu	Gly	Tyr	Trp	Glu	Ala	Trp	Arg	His	His	Cys	Gln	Gly	Lys
				125					130					135

Asp	Leu	Thr	Glu	Trp	Val	Asp	Gly	Cys	Asp	Phe
				140					145	

<210> 222  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 222  
gggatcatgt tgttggccct ggtc 24

<210> 223  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 223  
gcaaggcaga cccagtcagc cag 23

<210> 224  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 224  
ctgcctgcta ccctccaagt gaggccaagc tctacggtcg ttgtg 45

<210> 225  
<211> 2049  
<212> DNA  
<213> Homo sapiens

<400> 225  
agccgctgcc ccggggccggg cgcccgcggc ggcaccatga gtccccgctc 50  
gtgcctgcgt tcgctgcgcc tctcgtctt cgcggtcttc tcagccgccg 100  
cgagcaactg gctgtacctg gccaaagtgt cgtcgggtggg gagcatctca 150  
gaggaggaga cgtgcgagaa actcaagggc ctgatccaga ggcaggtgca 200  
gatgtgcaag cggaacctgg aagtcattga ctcggtgcgc cgcggtgccc 250  
agctggccat tgaggagtgc cagtaccagt tccggaaccg gcgctggaac 300  
tgctccacac tcgactcctt gcccgctcttc ggcaaggtgg tgacgcaagg 350  
gactcgggag gcggccttcg tgtacgcat ctcttcggca ggtgtggcct 400  
ttgcagtgac gcgggcgtgc agcagtgggg agctggagaa gtgcggctgt 450

gacaggacag tgcattgggt cagccacag ggcttccagt ggtcaggatg 500  
ctctgacaac atcgctacg gtgtggcctt ctcacagtcg tttgtggatg 550  
tgctggagag aagcaagggg gcctcgtcca gcagagccct catgaacctc 600  
cacaacaatg aggccggcag gaaggccatc ctgacacaca tgcgggtgga 650  
atgcaagtgc cacgggggtg caggctcctg tgaggtaaag acgtgctggc 700  
gagccgtgcc gcccttccgc cagggtgggtc acgcactgaa ggagaagttt 750  
gatggtgcca ctgaggtgga gccacgccgc gtgggctcct ccagggcact 800  
ggtaccacgc aacgcacagt tcaagccgca cacagatgag gacctggtgt 850  
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ctgggcacga ggggccgcac atgcaacaag acgtccaagg ccatcgacgg 950  
ctgtgagctg ctgtgctgtg gccggggctt ccacacggcg cagggtggagc 1000  
tggtgaacg ctgcagctgc aaattccact ggtgctgctt cgtcaagtgc 1050  
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ctagccctgc gccggcaacc acctagtggc ccagggaagg ccgataattt 1150  
aaacagtctc ccaccaccta cccaagaga tactggttgt attttttgtt 1200  
ctggttttgt ttttgggtcc tcatgttatt tattgccgaa accaggcagg 1250  
caacccaag ggcaccaacc agggcctccc caaagcctgg gcctttgtgg 1300  
ctgccactga ccaaagggac cttgctcgtg ccgctggctg cccgcatgtg 1350  
gtgccactg accactcagt tggtatctgt gtccgttttt ctacttgacg 1400  
acctaaagggt gagtaacaag gagtattacc accacatggc tactgaccgt 1450  
gtcatcgggg aagagggggc cttatggcag ggaaaatagg taccgacttg 1500  
atggaagtca caccctctgg aaaaaagaac tcttaactct ccagcacaca 1550  
tacacatgga ctctggcag cttgagccta gaagccatgt ctctcaaagt 1600  
ccctgagaaa gggaacaagc agataccagg tcaagggcac caggttcatt 1650  
tcagccctta catggacagc tagaggttcg atatctgtgg gtccttccag 1700  
gcaagaagag ggagatgaga gcaagagacg actgaagtcc caccctagaa 1750  
cccagcctgc cccagcctgc ccctgggaag aggaaactta accactcccc 1800  
agaccacct aggcaggcat ataggctgcc atcctggacc agggatcccc 1850

gctgtgcctt tgcagtcac cccgagtcac ctttcacagc gctgttcctc 1900  
catgaaactg aaaaacacac acacacacac acacacacac acacacacac 1950  
acacacacac ggacacacac acacacctgc gagagagagg gaggaaaggg 2000  
ctgtgccttt gcagtcacgc ccgagtcacc tttcacagca ctgttcctc 2049

<210> 226  
<211> 351  
<212> PRT  
<213> Homo sapiens

<400> 226

Met	Ser	Pro	Arg	Ser	Cys	Leu	Arg	Ser	Leu	Arg	Leu	Leu	Val	Phe	1	5	10	15
Ala	Val	Phe	Ser	Ala	Ala	Ala	Ser	Asn	Trp	Leu	Tyr	Leu	Ala	Lys	20	25	30	
Leu	Ser	Ser	Val	Gly	Ser	Ile	Ser	Glu	Glu	Glu	Thr	Cys	Glu	Lys	35	40	45	
Leu	Lys	Gly	Leu	Ile	Gln	Arg	Gln	Val	Gln	Met	Cys	Lys	Arg	Asn	50	55	60	
Leu	Glu	Val	Met	Asp	Ser	Val	Arg	Arg	Gly	Ala	Gln	Leu	Ala	Ile	65	70	75	
Glu	Glu	Cys	Gln	Tyr	Gln	Phe	Arg	Asn	Arg	Arg	Trp	Asn	Cys	Ser	80	85	90	
Thr	Leu	Asp	Ser	Leu	Pro	Val	Phe	Gly	Lys	Val	Val	Thr	Gln	Gly	95	100	105	
Thr	Arg	Glu	Ala	Ala	Phe	Val	Tyr	Ala	Ile	Ser	Ser	Ala	Gly	Val	110	115	120	
Ala	Phe	Ala	Val	Thr	Arg	Ala	Cys	Ser	Ser	Gly	Glu	Leu	Glu	Lys	125	130	135	
Cys	Gly	Cys	Asp	Arg	Thr	Val	His	Gly	Val	Ser	Pro	Gln	Gly	Phe	140	145	150	
Gln	Trp	Ser	Gly	Cys	Ser	Asp	Asn	Ile	Ala	Tyr	Gly	Val	Ala	Phe	155	160	165	
Ser	Gln	Ser	Phe	Val	Asp	Val	Arg	Glu	Arg	Ser	Lys	Gly	Ala	Ser	170	175	180	
Ser	Ser	Arg	Ala	Leu	Met	Asn	Leu	His	Asn	Asn	Glu	Ala	Gly	Arg	185	190	195	
Lys	Ala	Ile	Leu	Thr	His	Met	Arg	Val	Glu	Cys	Lys	Cys	His	Gly	200	205	210	
Val	Ser	Gly	Ser	Cys	Glu	Val	Lys	Thr	Cys	Trp	Arg	Ala	Val	Pro				

215	220	225
Pro Phe Arg Gln Val Gly His Ala Leu Lys Glu Lys Phe Asp Gly		
230	235	240
Ala Thr Glu Val Glu Pro Arg Arg Val Gly Ser Ser Arg Ala Leu		
245	250	255
Val Pro Arg Asn Ala Gln Phe Lys Pro His Thr Asp Glu Asp Leu		
260	265	270
Val Tyr Leu Glu Pro Ser Pro Asp Phe Cys Glu Gln Asp Met Arg		
275	280	285
Ser Gly Val Leu Gly Thr Arg Gly Arg Thr Cys Asn Lys Thr Ser		
290	295	300
Lys Ala Ile Asp Gly Cys Glu Leu Leu Cys Cys Gly Arg Gly Phe		
305	310	315
His Thr Ala Gln Val Glu Leu Ala Glu Arg Cys Ser Cys Lys Phe		
320	325	330
His Trp Cys Cys Phe Val Lys Cys Arg Gln Cys Gln Arg Leu Val		
335	340	345
Glu Leu His Thr Cys Arg		
350		

<210> 227  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 227  
 gctgcagctg caaattccac tgg 23

<210> 228  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 228  
 tgggtgggaga ctgttttaa tgcggcc 28

<210> 229  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<223> Synthetic oligonucleotide probe

<400> 229

tgcttcgtca agtgccggca gtgccagcgg ctctgtggagt t 41

<210> 230

<211> 1355

<212> DNA

<213> Homo sapiens

<400> 230

cggacgcgtg ggccggacgc tgggcccgcg cgtgggcgga cgcgtgggct 50  
gggtgcctgc atcgccatgg acaccaccag gtacagcaag tggggcggca 100  
gctccgagga ggtccccgga gggccctggg gacgctgggt gcactggagc 150  
aggagacccc tcttcttggc cctggctgtc ctggtcacca cagtcctttg 200  
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cactgagctg ttccggggcg tggaggccgt gaggctccag aacaactcct 550  
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cagcttcagc cactggaacc agggagagcc caatgacgct tgggggcgcg 850  
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gacagcgaga aggacggctg gatctgtgag aaaaggcaca actgctgacc 950  
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tcctcatcca ccgtgctga gtctcagaaa cacttggccc aacatagccc 1100  
tgtccagccc agtgccctggg ctctgggacc tccatgccga cctcatccta 1150

actccactca cgcagaccca acctaacctc cactagctcc aaaatccctg 1200  
 ctctgcgctc ccogtgatat gcctccactt ctctccctaa ccaagggttag 1250  
 gtgactgagg actggagctg tttggttttc tcgcattttc caccaaactg 1300  
 gaagctgttt ttgcagcctg aggaagcatc aataaatatt tgagaaatga 1350  
 aaaaa 1355

<210> 231

<211> 293

<212> PRT

<213> Homo sapiens

<400> 231

Met	Asp	Thr	Thr	Arg	Tyr	Ser	Lys	Trp	Gly	Gly	Ser	Ser	Glu	Glu	1	5	10	15
Val	Pro	Gly	Gly	Pro	Trp	Gly	Arg	Trp	Val	His	Trp	Ser	Arg	Arg	20	25	30	
Pro	Leu	Phe	Leu	Ala	Leu	Ala	Val	Leu	Val	Thr	Thr	Val	Leu	Trp	35	40	45	
Ala	Val	Ile	Leu	Ser	Ile	Leu	Leu	Ser	Lys	Ala	Ser	Thr	Glu	Arg	50	55	60	
Ala	Ala	Leu	Leu	Asp	Gly	His	Asp	Leu	Leu	Arg	Thr	Asn	Ala	Ser	65	70	75	
Lys	Gln	Thr	Ala	Ala	Leu	Gly	Ala	Leu	Lys	Glu	Glu	Val	Gly	Asp	80	85	90	
Cys	His	Ser	Cys	Cys	Ser	Gly	Thr	Gln	Ala	Gln	Leu	Gln	Thr	Thr	95	100	105	
Arg	Ala	Glu	Leu	Gly	Glu	Ala	Gln	Ala	Lys	Leu	Met	Glu	Gln	Glu	110	115	120	
Ser	Ala	Leu	Arg	Glu	Leu	Arg	Glu	Arg	Val	Thr	Gln	Gly	Leu	Ala	125	130	135	
Glu	Ala	Gly	Arg	Gly	Arg	Glu	Asp	Val	Arg	Thr	Glu	Leu	Phe	Arg	140	145	150	
Ala	Leu	Glu	Ala	Val	Arg	Leu	Gln	Asn	Asn	Ser	Cys	Glu	Pro	Cys	155	160	165	
Pro	Thr	Ser	Trp	Leu	Ser	Phe	Glu	Gly	Ser	Cys	Tyr	Phe	Phe	Ser	170	175	180	
Val	Pro	Lys	Thr	Thr	Trp	Ala	Ala	Ala	Gln	Asp	His	Cys	Ala	Asp	185	190	195	
Ala	Ser	Ala	His	Leu	Val	Ile	Val	Gly	Gly	Leu	Asp	Glu	Gln	Gly	200	205	210	

Phe	Leu	Thr	Arg	Asn	Thr	Arg	Gly	Arg	Gly	Tyr	Trp	Leu	Gly	Leu	215	220	225
Arg	Ala	Val	Arg	His	Leu	Gly	Lys	Val	Gln	Gly	Tyr	Gln	Trp	Val	230	235	240
Asp	Gly	Val	Ser	Leu	Ser	Phe	Ser	His	Trp	Asn	Gln	Gly	Glu	Pro	245	250	255
Asn	Asp	Ala	Trp	Gly	Arg	Glu	Asn	Cys	Val	Met	Met	Leu	His	Thr	260	265	270
Gly	Leu	Trp	Asn	Asp	Ala	Pro	Cys	Asp	Ser	Glu	Lys	Asp	Gly	Trp	275	280	285
Ile	Cys	Glu	Lys	Arg	His	Asn	Cys								290		

<210> 232  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 232  
 gcgagaactg tgatcatgatg ctgc 24

<210> 233  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 233  
 gtttctgaga ctcagcagcg gtgg 24

<210> 234  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 234  
 caccgtgtga cagcgagaag gacggctgga tctgtgagaa aaggcacaac 50

<210> 235  
 <211> 1847  
 <212> DNA  
 <213> Homo sapiens



<400> 235

gccaggggaa gaggtgatc cgacccgggg aaggtcgctg ggcagggcga 50  
gttgggaaag cggcagcccc cgccgcccc gcagcccctt ctctccttt 100  
ctcccacgtc ctatctgcct ctcgctggag gccaggccgt gcagcatcga 150  
agacaggagg aactggagcc tcattggccg gcccgggcg ccggcctcgg 200  
gcttaaatag gagctccggg ctctggctgg gacccgaccg ctgccggccg 250  
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cctgggcaag gccctctgcg ctctcctcct ggccactctc ggcgccgcg 350  
gccagcctct tgggggagag tccatctgtt ccgccagagc cccggccaaa 400  
tacagcatca ccttcacggg caagtggagc cagacggcct tccccaagca 450  
gtaccccctg ttccgcccc ctgcgcagtg gtcttcgctg ctgggggccc 500  
cgcatagctc cgactacagc atgtggagga agaaccagta cgtcagtaac 550  
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gatcgaggcg gcgggggagg cgctgcagag cgtgcacgag gtgttttcgg 650  
cgcccgccgt cccagcggc accgggcaga cgtcggcgga gctggagggtg 700  
cagcgcaggc actcgctggt ctcgtttggt gtgcgcacgtg tgcccagccc 750  
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actaccgcg gctgaaggcc ctgcctccca tcgccagggt gacactgctg 1000  
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 gtctgtcttc agcctcctcc tcctgcagga taaagtcac cccaaggctc 1550  
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 tgctcacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1847

<210> 236

<211> 331

<212> PRT

<213> Homo sapiens

<400> 236

Met	Glu	Asn	Pro	Ser	Pro	Ala	Ala	Ala	Leu	Gly	Lys	Ala	Leu	Cys	1	5	10	15
Ala	Leu	Leu	Leu	Ala	Thr	Leu	Gly	Ala	Ala	Gly	Gln	Pro	Leu	Gly	20	25	30	
Gly	Glu	Ser	Ile	Cys	Ser	Ala	Arg	Ala	Pro	Ala	Lys	Tyr	Ser	Ile	35	40	45	
Thr	Phe	Thr	Gly	Lys	Trp	Ser	Gln	Thr	Ala	Phe	Pro	Lys	Gln	Tyr	50	55	60	
Pro	Leu	Phe	Arg	Pro	Pro	Ala	Gln	Trp	Ser	Ser	Leu	Leu	Gly	Ala	65	70	75	
Ala	His	Ser	Ser	Asp	Tyr	Ser	Met	Trp	Arg	Lys	Asn	Gln	Tyr	Val	80	85	90	
Ser	Asn	Gly	Leu	Arg	Asp	Phe	Ala	Glu	Arg	Gly	Glu	Ala	Trp	Ala	95	100	105	
Leu	Met	Lys	Glu	Ile	Glu	Ala	Ala	Gly	Glu	Ala	Leu	Gln	Ser	Val	110	115	120	
His	Glu	Val	Phe	Ser	Ala	Pro	Ala	Val	Pro	Ser	Gly	Thr	Gly	Gln	125	130	135	
Thr	Ser	Ala	Glu	Leu	Glu	Val	Gln	Arg	Arg	His	Ser	Leu	Val	Ser	140	145	150	
Phe	Val	Val	Arg	Ile	Val	Pro	Ser	Pro	Asp	Trp	Phe	Val	Gly	Val	155	160	165	

Asp Ser Leu Asp Leu Cys Asp Gly Asp Arg Trp Arg Glu Gln Ala	170	175	180
Ala Leu Asp Leu Tyr Pro Tyr Asp Ala Gly Thr Asp Ser Gly Phe	185	190	195
Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp Thr Val	200	205	210
Thr Glu Ile Thr Ser Ser Ser Pro Ser His Pro Ala Asn Ser Phe	215	220	225
Tyr Tyr Pro Arg Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr	230	235	240
Leu Leu Arg Leu Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala	245	250	255
Pro Val Leu Pro Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser	260	265	270
Val Pro Glu Thr Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser	275	280	285
Trp Gly Leu Cys Gly Gly His Cys Gly Arg Leu Gly Thr Lys Ser	290	295	300
Arg Thr Arg Tyr Val Arg Val Gln Pro Ala Asn Asn Gly Ser Pro	305	310	315
Cys Pro Glu Leu Glu Glu Glu Ala Glu Cys Val Pro Asp Asn Cys	320	325	330

Val

<210> 237  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 237  
 cagcactgcc aggggaagag gg 22

<210> 238  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 238  
 caggactcgc tacgtccg 18

<210> 239  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 239  
cagccccttc tcctcctttc tccc 24

<210> 240  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 240  
gcagttatca gggacgcact cagcc 25

<210> 241  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 241  
ccagcgagag gcagatag 18

<210> 242  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 242  
cggtcacccgt gtccctgcggg atg 23

<210> 243  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 243  
cagccccttc tcctcctttc tcccacgtcc tatctgcctc tc 42

<210> 244

<211> 1894  
<212> DNA  
<213> Homo sapiens

<400> 244

ggcggcgctcc gtgaggggct cctttgggca ggggtagtgt ttggtgtccc 50  
tgtcttgctg gatattgaca aactgaagct ttcctgcacc actggactta 100  
aggaagagtg tactcgtagg cggacagctt tagtggccgg ccggccgctc 150  
tcatcccccg taaggagcag agtcctttgt actgaccaag atgagcaaca 200  
tctacatcca ggagcctccc acgaatggga aggttttatt gaaaactaca 250  
gctggagata ttgacataga gttgtggtcc aaagaagctc cttaaagcttg 300  
cagaaatfff atccaactff gtttggaagc ttattatgac aataccatff 350  
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acagggagtg gtggagagtc tatctatgga gcgccattca aagatgaatt 450  
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gaccacataa tccacacaaa ataaaaagct gtgaggttff gtttaatcct 700  
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 tgttttgcaa attgtggaat gatgtaagca aatgcttttg gttactggta 1800  
 catgtgtttt ttcctagctg accttttata ttgctaaatc tgaaataaaa 1850  
 taactttcct tccacaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1894

<210> 245  
 <211> 472  
 <212> PRT  
 <213> Homo sapiens

<400> 245  
 Met Ser Asn Ile Tyr Ile Gln Glu Pro Pro Thr Asn Gly Lys Val  
     1                    5                    10                    15  
 Leu Leu Lys Thr Thr Ala Gly Asp Ile Asp Ile Glu Leu Trp Ser  
                     20                    25                    30  
 Lys Glu Ala Pro Lys Ala Cys Arg Asn Phe Ile Gln Leu Cys Leu  
                     35                    40                    45  
 Glu Ala Tyr Tyr Asp Asn Thr Ile Phe His Arg Val Val Pro Gly  
                     50                    55                    60  
 Phe Ile Val Gln Gly Gly Asp Pro Thr Gly Thr Gly Ser Gly Gly  
                     65                    70                    75  
 Glu Ser Ile Tyr Gly Ala Pro Phe Lys Asp Glu Phe His Ser Arg  
                     80                    85                    90  
 Leu Arg Phe Asn Arg Arg Gly Leu Val Ala Met Ala Asn Ala Gly  
                     95                    100                    105  
 Ser His Asp Asn Gly Ser Gln Phe Phe Phe Thr Leu Gly Arg Ala  
                     110                    115                    120  
 Asp Glu Leu Asn Asn Lys His Thr Ile Phe Gly Lys Val Thr Gly  
                     125                    130                    135

Asp Thr Val Tyr Asn Met Leu Arg Leu Ser Glu Val Asp Ile Asp	140	145	150
Asp Asp Glu Arg Pro His Asn Pro His Lys Ile Lys Ser Cys Glu	155	160	165
Val Leu Phe Asn Pro Phe Asp Asp Ile Ile Pro Arg Glu Ile Lys	170	175	180
Arg Leu Lys Lys Glu Lys Pro Glu Glu Glu Val Lys Lys Leu Lys	185	190	195
Pro Lys Gly Thr Lys Asn Phe Ser Leu Leu Ser Phe Gly Glu Glu	200	205	210
Ala Glu Glu Glu Glu Glu Glu Val Asn Arg Val Ser Gln Ser Met	215	220	225
Lys Gly Lys Ser Lys Ser Ser His Asp Leu Leu Lys Asp Asp Pro	230	235	240
His Leu Ser Ser Val Pro Val Val Glu Ser Glu Lys Gly Asp Ala	245	250	255
Pro Asp Leu Val Asp Asp Gly Glu Asp Glu Ser Ala Glu His Asp	260	265	270
Glu Tyr Ile Asp Gly Asp Glu Lys Asn Leu Met Arg Glu Arg Ile	275	280	285
Ala Lys Lys Leu Lys Lys Asp Thr Ser Ala Asn Val Lys Ser Ala	290	295	300
Gly Glu Gly Glu Val Glu Lys Lys Ser Val Ser Arg Ser Glu Glu	305	310	315
Leu Arg Lys Glu Ala Arg Gln Leu Lys Arg Glu Leu Leu Ala Ala	320	325	330
Lys Gln Lys Lys Val Glu Asn Ala Ala Lys Gln Ala Glu Lys Arg	335	340	345
Ser Glu Glu Glu Glu Ala Pro Pro Asp Gly Ala Val Ala Glu Tyr	350	355	360
Arg Arg Glu Lys Gln Lys Tyr Glu Ala Leu Arg Lys Gln Gln Ser	365	370	375
Lys Lys Gly Thr Ser Arg Glu Asp Gln Thr Leu Ala Leu Leu Asn	380	385	390
Gln Phe Lys Ser Lys Leu Thr Gln Ala Ile Ala Glu Thr Pro Glu	395	400	405
Asn Asp Ile Pro Glu Thr Glu Val Glu Asp Asp Glu Gly Trp Met	410	415	420

Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg Lys Val Lys Asp  
425 430 435

Ala Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr Asp Pro Arg  
440 445 450

Asn Pro Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys Leu Met  
455 460 465

Arg Glu Lys Lys Glu Arg Arg  
470

<210> 246

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

tgcgagatc ctactggcac aggg 24

<210> 247

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 247

cgagttagtc agagcatg 18

<210> 248

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 248

cagatggtgc tgttgccg 18

<210> 249

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 249

caactggaac aggaactgag atgtggatc 29

<210> 250



<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 250  
ctggttcagc agtgcaaggg tctg 24

<210> 251  
<211> 18  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 251  
cctctccgat taaaacgc 18

<210> 252  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 252  
gagaggactg gttgccatgg caaatgctgg ttctcatgat aatgg 45

<210> 253  
<211> 2456  
<212> DNA  
<213> Homo sapiens

<400> 253  
cgccgccgtt ggggctggaa gttcccgccca ggtccgtgcc gggcgagaga 50  
gatgctgccc ggcccgcctc ggctttgagg cgagagaagt gtcccagacc 100  
catttcgcct tgctgacggc gtcgagccct ggccagacat gtccacaggg 150  
ttctccttcg ggtccgggac tctggggtcc accaccgtgg ccgccggcgg 200  
gaccagcaca ggcggcggtt tctccttcgg aacgggaacg tctagcaacc 250  
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ctccgcctcc cgggttcaag cgagtctcct gcctcagcct ctgagtgtct 700  
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tgccacactg gctggatgca accacaacag cacacagatc ctggtaaact 1300  
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ggattttacc acaagagtgg gcatgaagct caaggagaag aagatggctt 1800  
tttgatgag tctgtaccag tctcaaagac ctgagaagca gaggcaattc 1850  
taagggtggc tatgcaggaa ggagccaaag aggggtttgc cccaccatc 1900

caggccctgg ggagactagc catggacata cctggggaca agagttctac 1950  
ccaccccagt ttagaactgc aggagctccc tgctgcctcc aggccaaagc 2000  
tagagctttt gcctgttgtg tgggacctgc actgcccttt ccagcctgac 2050  
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ctgtcaacac cacactgtgc tcagctctcc agcctcagga caacctcttt 2150  
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tcttatggga ggtcgacca gactgccact gcccctgtca ctgcacccag 2250  
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ttgggatctt ctctcccacc cacacttate tccccaggg ccactccaaa 2400  
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aaaaaa 2456

<210> 254

<211> 545

<212> PRT

<213> Homo sapiens

<400> 254

Met	Ser	Thr	Gly	Phe	Ser	Phe	Gly	Ser	Gly	Thr	Leu	Gly	Ser	Thr	1	5	10	15
Thr	Val	Ala	Ala	Gly	Gly	Thr	Ser	Thr	Gly	Gly	Val	Phe	Ser	Phe	20	25	30	
Gly	Thr	Gly	Thr	Ser	Ser	Asn	Pro	Ser	Val	Gly	Leu	Asn	Phe	Gly	35	40	45	
Asn	Leu	Gly	Ser	Thr	Ser	Thr	Pro	Ala	Thr	Thr	Ser	Ala	Pro	Ser	50	55	60	
Ser	Gly	Phe	Gly	Thr	Gly	Leu	Phe	Gly	Ser	Lys	Pro	Ala	Thr	Gly	65	70	75	
Phe	Thr	Leu	Gly	Gly	Thr	Asn	Thr	Gly	Ala	Leu	His	Thr	Lys	Arg	80	85	90	
Pro	Gln	Val	Val	Thr	Lys	Tyr	Gly	Thr	Leu	Gln	Gly	Lys	Gln	Met	95	100	105	
His	Val	Gly	Lys	Thr	Pro	Ile	Gln	Val	Phe	Leu	Gly	Val	Pro	Phe	110	115	120	
Ser	Arg	Pro	Pro	Leu	Gly	Ile	Leu	Arg	Phe	Ala	Pro	Pro	Glu	Pro	125	130	135	

Pro Glu Pro Trp	Lys Gly Ile Arg Asp	Ala Thr Thr Tyr Pro	Pro
140	145		150
Gly Trp Ser Leu	Ala Leu Ser Pro Gly	Trp Ser Ala Val Ala	Arg
155	160		165
Ser Arg Leu Thr	Ala Thr Ser Ala Ser	Arg Val Gln Ala Ser	Leu
170	175		180
Leu Pro Gln Pro	Leu Ser Val Trp Gly	Tyr Arg Cys Leu Gln	Glu
185	190		195
Ser Trp Gly Gln	Leu Ala Ser Met Tyr	Val Ser Thr Arg Glu	Arg
200	205		210
Tyr Lys Trp Leu	Arg Phe Ser Glu Asp	Cys Leu Tyr Leu Asn	Val
215	220		225
Tyr Ala Pro Ala	Arg Ala Pro Gly Asp	Pro Gln Leu Pro Val	Met
230	235		240
Val Trp Phe Pro	Gly Gly Ala Phe Ile	Val Gly Ala Ala Ser	Ser
245	250		255
Tyr Glu Gly Ser	Asp Leu Ala Ala Arg	Glu Lys Val Val Leu	Val
260	265		270
Phe Leu Gln His	Arg Leu Gly Ile Phe	Gly Phe Leu Ser Thr	Asp
275	280		285
Asp Ser His Ala	Arg Gly Asn Trp Gly	Leu Leu Asp Gln Met	Ala
290	295		300
Ala Leu Arg Trp	Val Gln Glu Asn Ile	Ala Ala Phe Gly Gly	Asp
305	310		315
Pro Gly Asn Val	Thr Leu Phe Gly Gln	Ser Ala Gly Ala Met	Ser
320	325		330
Ile Ser Gly Leu	Met Met Ser Pro Leu	Ala Ser Gly Leu Phe	His
335	340		345
Arg Ala Ile Ser	Gln Ser Gly Thr Ala	Leu Phe Arg Leu Phe	Ile
350	355		360
Thr Ser Asn Pro	Leu Lys Val Ala Lys	Lys Val Ala His Leu	Ala
365	370		375
Gly Cys Asn His	Asn Ser Thr Gln Ile	Leu Val Asn Cys Leu	Arg
380	385		390
Ala Leu Ser Gly	Thr Lys Val Met Arg	Val Ser Asn Lys Met	Arg
395	400		405
Phe Leu Gln Leu	Asn Phe Gln Arg Asp	Pro Glu Glu Ile Ile	Trp
410	415		420

Ser Met Ser Pro Val Val Asp Gly Val Val Ile Pro Asp Asp Pro	425	430	435
Leu Val Leu Leu Thr Gln Gly Lys Val Ser Ser Val Pro Tyr Leu	440	445	450
Leu Gly Val Asn Asn Leu Glu Phe Asn Trp Leu Leu Pro Tyr Asn	455	460	465
Ile Thr Lys Glu Gln Val Pro Leu Val Val Glu Glu Tyr Leu Asp	470	475	480
Asn Val Asn Glu His Asp Trp Lys Met Leu Arg Asn Arg Met Met	485	490	495
Asp Ile Val Gln Asp Ala Thr Phe Val Tyr Ala Thr Leu Gln Thr	500	505	510
Ala His Tyr His Arg Glu Thr Pro Met Met Gly Ile Cys Pro Ala	515	520	525
Gly His Ala Thr Thr Arg Met Lys Ser Thr Cys Ser Trp Ile Leu	530	535	540
Pro Gln Glu Trp Ala	545		

<210> 255  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 255  
 aggtgcctgc aggagtcctg ggg 23

<210> 256  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 256  
 ccacctcagg aagccgaaga tgcc 24

<210> 257  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 257  
gaacggtaca agtggctgcg cttcagcgag gactgtctgt acctg 45

<210> 258

<211> 2764

<212> DNA

<213> Homo sapiens

<400> 258

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actgccactg ctgtctgcct cgctgctggg cgggtcccag gctatggatg 100  
ggagattctg gatacgagtg caggagtcag tgatggtgcc ggagggcctg 150  
tgcatctctg tgccctgctc tttctcctac ccccgacaag actggacagg 200  
gtctacccca gcttatggct actggttcaa agcagtgact gagacaacca 250  
aggggtgctcc tgtggccaca aaccaccaga gtcgagaggt ggaaatgagc 300  
acccgggggc gattccagct cactggggat cccgccaagg ggaactgctc 350  
cttggtgatc agagacgcgc agatgcagga tgagtcacag tacttctttc 400  
gggtggagag aggaagctat gtgacatata atttcatgaa cgatgggttc 450  
tttctaaaag taacagtgtc cagcttcacg cccagacccc aggaccacaa 500  
caccgacctc acctgccatg tggacttctc cagaaagggg gtgagcgcac 550  
agaggaccgt ccgactccgt gtggcctatg cccccagaga ccttgttatc 600  
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tgtcccatc ctggaagccc aaaaaggcca gttcctgcgg ctctctctgtg 700  
ctgctgacag ccagccccct gccacactga gctgggtcct gcagaacaga 750  
gtcctctcct cgtcccatcc ctggggccct agaccctgg ggctggagct 800  
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acaggcttgg ctcccagcag cgagccctgg acctctctgt gcagtatcct 900  
ccagagaacc tgagagtgat ggtttcccaa gcaaacagga cagtcctgga 950  
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gcctggtctg tgtcacacac agcagcccc cagccaggct gagctggacc 1050  
cagaggggac aggttctgag cccctcccag ccctcagacc ccggggtcct 1100  
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ctcggcaccc actgggtcc cagcaogtct ctctcagcct ctccgtgcac 1200

tataagaagg gactcatctc aacggcattc tccaacggag cgtttctggg 1250  
aatcggcatc acggctcttc ttttctctg cctggccctg atcatcatga 1300  
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ccccctgggt cagaagcggg atcagaaaagc cacaccaaag agtcctcgga 1450  
cccctctcc accaggtgct ccctccccag aatcaaagaa gaaccagaaa 1500  
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tcgggagttc gagaccagcc tggccaactt ggtgaaaccc cgtctctact 1950  
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cccagcactt tgggaggcta aggtgggtg attgcttgag cccaggagtt 2200  
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gccacgagag tgacctctgg tcgtctcac tgctacactc ctgacagcac 2550  
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cccaaaaggg ggaggaatga ataatccacc ccttgtttag caaataagca 2650

agaaataacc ataaaagtgg gcaaccagca gctctaggcg ctgctcttgt 2700

ctatggagta gccattcttt tgttccttta ctttcttaat aaacttgctt 2750

tcaccttaaa aaaa 2764

<210> 259

<211> 544

<212> PRT

<213> Homo sapiens

<400> 259

Met	Leu	Leu	Pro	Leu	Leu	Leu	Ser	Ser	Leu	Leu	Gly	Gly	Ser	Gln
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Ala	Met	Asp	Gly	Arg	Phe	Trp	Ile	Arg	Val	Gln	Glu	Ser	Val	Met
				20					25					30

Val	Pro	Glu	Gly	Leu	Cys	Ile	Ser	Val	Pro	Cys	Ser	Phe	Ser	Tyr
				35					40					45

Pro	Arg	Gln	Asp	Trp	Thr	Gly	Ser	Thr	Pro	Ala	Tyr	Gly	Tyr	Trp
				50					55					60

Phe	Lys	Ala	Val	Thr	Glu	Thr	Thr	Lys	Gly	Ala	Pro	Val	Ala	Thr
				65					70					75

Asn	His	Gln	Ser	Arg	Glu	Val	Glu	Met	Ser	Thr	Arg	Gly	Arg	Phe
				80					85					90

Gln	Leu	Thr	Gly	Asp	Pro	Ala	Lys	Gly	Asn	Cys	Ser	Leu	Val	Ile
				95					100					105

Arg	Asp	Ala	Gln	Met	Gln	Asp	Glu	Ser	Gln	Tyr	Phe	Phe	Arg	Val
				110					115					120

Glu	Arg	Gly	Ser	Tyr	Val	Thr	Tyr	Asn	Phe	Met	Asn	Asp	Gly	Phe
				125					130					135

Phe	Leu	Lys	Val	Thr	Val	Leu	Ser	Phe	Thr	Pro	Arg	Pro	Gln	Asp
				140					145					150

His	Asn	Thr	Asp	Leu	Thr	Cys	His	Val	Asp	Phe	Ser	Arg	Lys	Gly
				155					160					165

Val	Ser	Ala	Gln	Arg	Thr	Val	Arg	Leu	Arg	Val	Ala	Tyr	Ala	Pro
				170					175					180

Arg	Asp	Leu	Val	Ile	Ser	Ile	Ser	Arg	Asp	Asn	Thr	Pro	Ala	Leu
				185					190					195

Glu	Pro	Gln	Pro	Gln	Gly	Asn	Val	Pro	Tyr	Leu	Glu	Ala	Gln	Lys
				200					205					210

Gly	Gln	Phe	Leu	Arg	Leu	Leu	Cys	Ala	Ala	Asp	Ser	Gln	Pro	Pro
				215					220					225



Ala Thr Leu Ser Trp Val Leu Gln Asn Arg Val Leu Ser Ser Ser	230	235	240
His Pro Trp Gly Pro Arg Pro Leu Gly Leu Glu Leu Pro Gly Val	245	250	255
Lys Ala Gly Asp Ser Gly Arg Tyr Thr Cys Arg Ala Glu Asn Arg	260	265	270
Leu Gly Ser Gln Gln Arg Ala Leu Asp Leu Ser Val Gln Tyr Pro	275	280	285
Pro Glu Asn Leu Arg Val Met Val Ser Gln Ala Asn Arg Thr Val	290	295	300
Leu Glu Asn Leu Gly Asn Gly Thr Ser Leu Pro Val Leu Glu Gly	305	310	315
Gln Ser Leu Cys Leu Val Cys Val Thr His Ser Ser Pro Pro Ala	320	325	330
Arg Leu Ser Trp Thr Gln Arg Gly Gln Val Leu Ser Pro Ser Gln	335	340	345
Pro Ser Asp Pro Gly Val Leu Glu Leu Pro Arg Val Gln Val Glu	350	355	360
His Glu Gly Glu Phe Thr Cys His Ala Arg His Pro Leu Gly Ser	365	370	375
Gln His Val Ser Leu Ser Leu Ser Val His Tyr Lys Lys Gly Leu	380	385	390
Ile Ser Thr Ala Phe Ser Asn Gly Ala Phe Leu Gly Ile Gly Ile	395	400	405
Thr Ala Leu Leu Phe Leu Cys Leu Ala Leu Ile Ile Met Lys Ile	410	415	420
Leu Pro Lys Arg Arg Thr Gln Thr Glu Thr Pro Arg Pro Arg Phe	425	430	435
Ser Arg His Ser Thr Ile Leu Asp Tyr Ile Asn Val Val Pro Thr	440	445	450
Ala Gly Pro Leu Ala Gln Lys Arg Asn Gln Lys Ala Thr Pro Asn	455	460	465
Ser Pro Arg Thr Pro Pro Pro Pro Gly Ala Pro Ser Pro Glu Ser	470	475	480
Lys Lys Asn Gln Lys Lys Gln Tyr Gln Leu Pro Ser Phe Pro Glu	485	490	495
Pro Lys Ser Ser Thr Gln Ala Pro Glu Ser Gln Glu Ser Gln Glu	500	505	510

Glu Leu His Tyr Ala Thr Leu Asn Phe Pro Gly Val Arg Pro Arg  
515 520 525

Pro Glu Ala Arg Met Pro Lys Gly Thr Gln Ala Asp Tyr Ala Glu  
530 535 540

Val Lys Phe Gln

<210> 260

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 260

caaagcctgc gcctggtctg tg 22

<210> 261

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 261

ttctggagcc cagagggtgc tgag 24

<210> 262

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 262

ggagctgcca cccattcaaa tggagcacga aggagagttc acctg 45

<210> 263

<211> 2857

<212> DNA

<213> Homo sapiens

<400> 263

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actgctgcgt tttatgttgg gaattcctct cctatggcct tgtcttgag 100

caacagaaaa ctctcaaaca aagaaagtca agcagccagt gcgatctcat 150

ttgagagtga agcgtggctg ggtgtggaac caattttttg taccagagga 200

aatgaatacg actagtcatc acatcggcca gctaagatct gatttagaca 250  
atggaaacaa ttctttccag tacaagcttt tgggagctgg agctggaagt 300  
acttttatca ttgatgaaag aacaggtgac atatatgcca tacagaagct 350  
tgatagagag gagcgatccc tctacatctt aagagcccag gtaatagaca 400  
tcgctactgg aagggctgtg gaacctgagt ctgagtttgt catcaaagtt 450  
tcggatatca atgacaatga accaaaattc ctagatgaac cttatgaggc 500  
cattgtacca gagatgtctc cagaaggaac attagttatc caggtgacag 550  
caagtgatgc tgacgatccc tcaagtggta ataatgctcg tctcctctac 600  
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taatcattca agccaaggac atgattggtc agccaggagc gttgtctgga 750  
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tcactacaag taactcactg gatcgtgaaa tcagtgcttg gtacaaccta 1350  
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 tatagtcaga gaaattttca tgaattattc catgaagtat tgtttccttt 2850  
 atttaaa 2857

<210> 264

<211> 772

<212> PRT

<213> Homo sapiens

<400> 264

Met	Asn	Cys	Tyr	Leu	Leu	Leu	Arg	Phe	Met	Leu	Gly	Ile	Pro	Leu		1	5	10	15
Leu	Trp	Pro	Cys	Leu	Gly	Ala	Thr	Glu	Asn	Ser	Gln	Thr	Lys	Lys		20	25	30	
Val	Lys	Gln	Pro	Val	Arg	Ser	His	Leu	Arg	Val	Lys	Arg	Gly	Trp		35	40	45	
Val	Trp	Asn	Gln	Phe	Phe	Val	Pro	Glu	Glu	Met	Asn	Thr	Thr	Ser		50	55	60	
His	His	Ile	Gly	Gln	Leu	Arg	Ser	Asp	Leu	Asp	Asn	Gly	Asn	Asn		65	70	75	
Ser	Phe	Gln	Tyr	Lys	Leu	Leu	Gly	Ala	Gly	Ala	Gly	Ser	Thr	Phe		80	85	90	
Ile	Ile	Asp	Glu	Arg	Thr	Gly	Asp	Ile	Tyr	Ala	Ile	Gln	Lys	Leu		95	100	105	
Asp	Arg	Glu	Glu	Arg	Ser	Leu	Tyr	Ile	Leu	Arg	Ala	Gln	Val	Ile		110	115	120	
Asp	Ile	Ala	Thr	Gly	Arg	Ala	Val	Glu	Pro	Glu	Ser	Glu	Phe	Val		125	130	135	
Ile	Lys	Val	Ser	Asp	Ile	Asn	Asp	Asn	Glu	Pro	Lys	Phe	Leu	Asp		140	145	150	
Glu	Pro	Tyr	Glu	Ala	Ile	Val	Pro	Glu	Met	Ser	Pro	Glu	Gly	Thr		155	160	165	
Leu	Val	Ile	Gln	Val	Thr	Ala	Ser	Asp	Ala	Asp	Asp	Pro	Ser	Ser		170	175	180	
Gly	Asn	Asn	Ala	Arg	Leu	Leu	Tyr	Ser	Leu	Leu	Gln	Gly	Gln	Pro		185	190	195	
Tyr	Phe	Ser	Val	Glu	Pro	Thr	Thr	Gly	Val	Ile	Arg	Ile	Ser	Ser		200	205	210	
Lys	Met	Asp	Arg	Glu	Leu	Gln	Asp	Glu	Tyr	Trp	Val	Ile	Ile	Gln		215	220	225	
Ala	Lys	Asp	Met	Ile	Gly	Gln	Pro	Gly	Ala	Leu	Ser	Gly	Thr	Thr		230	235	240	
Ser	Val	Leu	Ile	Lys	Leu	Ser	Asp	Val	Asn	Asp	Asn	Lys	Pro	Ile		245	250	255	
Phe	Lys	Glu	Ser	Leu	Tyr	Arg	Leu	Thr	Val	Ser	Glu	Ser	Ala	Pro		260	265	270	
Thr	Gly	Thr	Ser	Ile	Gly	Thr	Ile	Met	Ala	Tyr	Asp	Asn	Asp	Ile		275	280	285	

Gly Glu Asn Ala	Glu Met Asp Tyr Ser	Ile Glu Glu Asp Asp Ser	
	290	295	300
Gln Thr Phe Asp	Ile Ile Thr Asn His	Glu Thr Gln Glu Gly Ile	
	305	310	315
Val Ile Leu Lys	Lys Lys Val Asp Phe	Glu His Gln Asn His Tyr	
	320	325	330
Gly Ile Arg Ala	Lys Val Lys Asn His	His Val Pro Glu Gln Leu	
	335	340	345
Met Lys Tyr His	Thr Glu Ala Ser Thr	Thr Phe Ile Lys Ile Gln	
	350	355	360
Val Glu Asp Val	Asp Glu Pro Pro Leu	Phe Leu Leu Pro Tyr Tyr	
	365	370	375
Val Phe Glu Val	Phe Glu Glu Thr Pro	Gln Gly Ser Phe Val Gly	
	380	385	390
Val Val Ser Ala	Thr Asp Pro Asp Asn	Arg Lys Ser Pro Ile Arg	
	395	400	405
Tyr Ser Ile Thr	Arg Ser Lys Val Phe	Asn Ile Asn Asp Asn Gly	
	410	415	420
Thr Ile Thr Thr	Ser Asn Ser Leu Asp	Arg Glu Ile Ser Ala Trp	
	425	430	435
Tyr Asn Leu Ser	Ile Thr Ala Thr Glu	Lys Tyr Asn Ile Glu Gln	
	440	445	450
Ile Ser Ser Ile	Pro Leu Tyr Val Gln	Val Leu Asn Ile Asn Asp	
	455	460	465
His Ala Pro Glu	Phe Ser Gln Tyr Tyr	Glu Thr Tyr Val Cys Glu	
	470	475	480
Asn Ala Gly Ser	Gly Gln Val Ile Gln	Thr Ile Ser Ala Val Asp	
	485	490	495
Arg Asp Glu Ser	Ile Glu Glu His His	Phe Tyr Phe Asn Leu Ser	
	500	505	510
Val Glu Asp Thr	Asn Asn Ser Ser Phe	Thr Ile Ile Asp Asn Gln	
	515	520	525
Asp Asn Thr Ala	Val Ile Leu Thr Asn	Arg Thr Gly Phe Asn Leu	
	530	535	540
Gln Glu Glu Pro	Val Phe Tyr Ile Ser	Ile Leu Ile Ala Asp Asn	
	545	550	555
Gly Ile Pro Ser	Leu Thr Ser Thr Asn	Thr Leu Thr Ile His Val	
	560	565	570

Cys	Asp	Cys	Gly	Asp	Ser	Gly	Ser	Thr	Gln	Thr	Cys	Gln	Tyr	Gln	575	580	585
Glu	Leu	Val	Leu	Ser	Met	Gly	Phe	Lys	Thr	Glu	Val	Ile	Ile	Ala	590	595	600
Ile	Leu	Ile	Cys	Ile	Met	Ile	Ile	Phe	Gly	Phe	Ile	Phe	Leu	Thr	605	610	615
Leu	Gly	Leu	Lys	Gln	Arg	Arg	Lys	Gln	Ile	Leu	Phe	Pro	Glu	Lys	620	625	630
Ser	Glu	Asp	Phe	Arg	Glu	Asn	Ile	Phe	Gln	Tyr	Asp	Asp	Glu	Gly	635	640	645
Gly	Gly	Glu	Glu	Asp	Thr	Glu	Ala	Phe	Asp	Ile	Ala	Glu	Leu	Arg	650	655	660
Ser	Ser	Thr	Ile	Met	Arg	Glu	Arg	Lys	Thr	Arg	Lys	Thr	Thr	Ser	665	670	675
Ala	Glu	Ile	Arg	Ser	Leu	Tyr	Arg	Gln	Ser	Leu	Gln	Val	Gly	Pro	680	685	690
Asp	Ser	Ala	Ile	Phe	Arg	Lys	Phe	Ile	Leu	Glu	Lys	Leu	Glu	Glu	695	700	705
Ala	Asn	Thr	Asp	Pro	Cys	Ala	Pro	Pro	Phe	Asp	Ser	Leu	Gln	Thr	710	715	720
Tyr	Ala	Phe	Glu	Gly	Thr	Gly	Ser	Leu	Ala	Gly	Ser	Leu	Ser	Ser	725	730	735
Leu	Glu	Ser	Ala	Val	Ser	Asp	Gln	Asp	Glu	Ser	Tyr	Asp	Tyr	Leu	740	745	750
Asn	Glu	Leu	Gly	Pro	Arg	Phe	Lys	Arg	Leu	Ala	Cys	Met	Phe	Gly	755	760	765
Ser	Ala	Val	Gln	Ser	Asn	Asn									770		

<210> 265

<211> 349

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 24, 60, 141, 226, 228, 249, 252

<223> unknown base

<400> 265

atttcaaggc cagccatatt tttntgttga accaacaaca ggagtcataa 50

gaatatttttn taaaatggat agagaactgc aagatgagta ttgggtaatc 100

attcaagcca aggacatgat tggtcagcca ggagcgttgt ntggaacaac 150  
aagtgtatta attaaacttt cagatgttaa tgacaataag cctatatatta 200  
aagaaagttt ataccgcttg actgtntntg aatctgcacc cactgggant 250  
tntataggaa caatcatggc atatgataat gacataggag agaatgcaga 300  
aatggattac agcattgaag aggatgattc gcaaacattt gacattatt 349

<210> 266

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 266

cttgactgtc tctgaatctg ccccc 25

<210> 267

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 267

aagtgggtgga agcctccagt gtgg 24

<210> 268

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 268

ccactacggt attagagcaa aagttaaaaa ccatcatggt tcctggagca 50

gc 52

<210> 269

<211> 2747

<212> DNA

<213> Homo sapiens

<400> 269

gcaacctcag cttctagtat ccagactcca gcgcgcgcgc gggcgcggaac 50

cccaaccccg acccagagct tctccagcgg cggcgccagcg agcagggctc 100

cccgcccttaa cttcctccgc ggggccccagc caccttcggg agtccggggtt 150



gcccacctgc aaactctccg ctttctgcac ctgccacccc tgagccagcg 200  
cgggcccccg agcgagtcac ggccaacgcg gggctgcagc tgttgggctt 250  
cattctcgcc ttcttgggat ggatcggcgc catcgtcagc actgccctgc 300  
cccagtggag gatttactcc tatgccggcg acaacatcgt gaccgcccag 350  
gccatgtacg aggggctgtg gatgtcctgc gtgtcgcaga gcaccgggca 400  
gatccagtgc aaagtctttg actccttgct gaatctgagc agcacattgc 450  
aagcaacccg tgccttgatg gtggttggca tcctcctggg agtgatagca 500  
atctttgtgg ccaccgttgg catgaagtgt atgaagtgt tggagacga 550  
tgaggtgcag aagatgagga tggctgtcat tgggggtgcg atatttcttc 600  
ttgcaggtct ggctatttta gttgccacag catggtatgg caatagaatc 650  
gttcaagaat tctatgaccc tatgaccca gtcaatgcca ggtacgaatt 700  
tggtcaggct ctcttactg gctgggctgc tgcttctctc tgccttctgg 750  
gaggtgccct actttgctgt tcctgtcccc gaaaaacaac ctcttaccga 800  
acaccaaggc cctatccaaa acctgcacct tccagcggga aagactacgt 850  
gtgacacaga ggcaaaagga gaaaatcatg ttgaaacaaa ccgaaaatgg 900  
acattgagat actatcatta acattaggac cttagaattt tgggtattgt 950  
aatctgaagt atggtattac aaaacaaaca aacaaacaaa aaacccatgt 1000  
gttaaaatac tcagtgctaa acatggctta atcttatttt atcttctttc 1050  
ctcaatatag gaggaagat ttttccattt gtattactgc ttcccattga 1100  
gtaatcatalc tcaaatgggg gaaggggtgc tccttaaata tatatagata 1150  
tgtatatata catgtttttc tattaataat agacagtaaa atactattct 1200  
cattatgttg atactagcat acttaaaata tctctaaaat aggtaaatgt 1250  
atttaattcc atattgatga agatgtttat tgggtatattt tctttttcgt 1300  
ccttatatac atatgtaaca gtcaaatac atttactctt cttcattagc 1350  
tttgggtgcc tttgccacaa gacctagcct aatttaccga ggatgaattc 1400  
tttcaattct tcatgctgc cttttcata tacttatttt attttttacc 1450  
ataatcttat agcacttgca tcgttattaa gcccttattt gttttgtgtt 1500  
tcattgtct ctatctctg aatctaacac atttcatagc ctacatttta 1550  
gtttctaaag ccaagaagaa ttattacaa atcagaactt tggaggcaaa 1600

tctttctgca tgaccaaagt gataaattcc tggtgacctt cccacacaat 1650  
ccctgtactc tgacccatag cactcttggt tgctttgaaa atatttgtcc 1700  
aattgagtag ctgcatgctg ttcccccagg tggtgtaaca caactttatt 1750  
gattgaattt ttaagctact tattcatagt tttatatccc cctaaactac 1800  
ctttttgttc ccattcctt aattgtattg ttttccaag tgtaattatc 1850  
atgcgtttta tatcttcta ataagggtg gtctgtttgt ctgaacaaag 1900  
tgctagactt tctggagtga taatctggtg acaaatttc tctctgtagc 1950  
tgtaagcaag tcacttaatc tttctacctc ttttttctat ctgccaaatt 2000  
gagataatga tacttaacca gttagaagag gtagtgtgaa tattaattag 2050  
tttatattac tcttattctt tgaacatgaa ctatgcctat gtagtgtctt 2100  
tatttgctca gctggctgag aactgaaga agtcactgaa caaacctac 2150  
acacgtacct tcatgtgatt cactgccttc ctctctctac cagtctattt 2200  
ccactgaaca aaacctacac acataccttc atgtggttca gtgccttcct 2250  
ctctctacca gtctatttcc actgaacaaa acctacgcac ataccttcat 2300  
gtggctcagt gccttcctct ctctaccagt ctatttccat tctttcagct 2350  
gtgtctgaca tggttggtct ctgttccatt ttaacaactg ctcttacttt 2400  
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aggggtgttg cactggtgtc tggagacctg gatttgagtc ttggtgctat 2500  
caatcacctg ctgtgtttga gcaaggcatt tggctgctgt aagcttattg 2550  
cttcatctgt aagcgggtgt ttgtaattcc tgatcttccc acctcacagt 2600  
gatgttggtg ggatccagtg agatagaata catgtaagtg tggttttgta 2650  
atttaaaaag tgctatacta agggaaagaa ttgaggaatt aactgcatac 2700  
gttttggtgt tgcttttcaa atgtttgaaa ataaaaaaaa tgtaag 2747

<210> 270

<211> 211

<212> PRT

<213> Homo sapiens

<400> 270

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1				5					10					15

Leu Gly Trp Ile Gly Ala Ile Val Ser Thr Ala Leu Pro Gln Trp

20										25					30				
Arg	Ile	Tyr	Ser	Tyr	Ala	Gly	Asp	Asn	Ile	Val	Thr	Ala	Gln	Ala					
				35					40					45					
Met	Tyr	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Ser	Gln	Ser	Thr	Gly					
				50					55					60					
Gln	Ile	Gln	Cys	Lys	Val	Phe	Asp	Ser	Leu	Leu	Asn	Leu	Ser	Ser					
				65					70					75					
Thr	Leu	Gln	Ala	Thr	Arg	Ala	Leu	Met	Val	Val	Gly	Ile	Leu	Leu					
				80					85					90					
Gly	Val	Ile	Ala	Ile	Phe	Val	Ala	Thr	Val	Gly	Met	Lys	Cys	Met					
				95					100					105					
Lys	Cys	Leu	Glu	Asp	Asp	Glu	Val	Gln	Lys	Met	Arg	Met	Ala	Val					
				110					115					120					
Ile	Gly	Gly	Ala	Ile	Phe	Leu	Leu	Ala	Gly	Leu	Ala	Ile	Leu	Val					
				125					130					135					
Ala	Thr	Ala	Trp	Tyr	Gly	Asn	Arg	Ile	Val	Gln	Glu	Phe	Tyr	Asp					
				140					145					150					
Pro	Met	Thr	Pro	Val	Asn	Ala	Arg	Tyr	Glu	Phe	Gly	Gln	Ala	Leu					
				155					160					165					
Phe	Thr	Gly	Trp	Ala	Ala	Ala	Ser	Leu	Cys	Leu	Leu	Gly	Gly	Ala					
				170					175					180					
Leu	Leu	Cys	Cys	Ser	Cys	Pro	Arg	Lys	Thr	Thr	Ser	Tyr	Pro	Thr					
				185					190					195					
Pro	Arg	Pro	Tyr	Pro	Lys	Pro	Ala	Pro	Ser	Ser	Gly	Lys	Asp	Tyr					
				200					205					210					

Val

<210> 271

<211> 564

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 21, 69, 163, 434, 436, 444

<223> unknown base

<400> 271

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ggatggatcg ggcctatent cacactgccc ttccccagtg gaggatttta 100

ctccctatgc tggcgacaac atcgtgaccg cccagcccat gtacgagggg 150

ctgtggatgt ccngcgtgtc gcagagcacc gggcagatcc agtgcaaagt 200  
ctttgactcc ttgctgaatc tgagcagcac attgcaagca acccgtgcct 250  
tgatgggtgtg tggcatcctc ctgggagtga tagcaatctt tgtggcacc 300  
gttggcatga agtgtatgaa gtgcttggaa gacgatgagg tgcagaagat 350  
gaggatggct gtcattgggg gcgcgatatt tcttcttgca ggtctggcta 400  
ttttagttgc cacagcatgg tatggcaata gaancnttca acanttctat 450  
gacctatga cccagtcaa tgccaggtac gaatttggc aggctctctt 500  
cactggctgg gctgctgctt ctctctgcct tctgggagg ggcctacttt 550  
gctgttcttg tccc 564

<210> 272

<211> 498

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 49, 102, 141, 147, 171, 324-325, 339-341

<223> unknown base

<400> 272

acccttgacc caacgcggcc ccccgaccgn ttcattggcca aacgcgggnc 50

tccagctgtt gggcttcatt ctccccctcc tgggatggac cggcgcccat 100

cntcagcact gccctgcccc agtggaggat ttactcctat nccggcnaca 150

acatcgtgac cgcccaggcc ntgtacgagg ggctgtggat gtcttgctg 200

tgcagagca ccgggcagat ccagtgcaaa gtctttgact cccttgctga 250

atctgagcag cacattgcaa gcaaccctg ccttgatggt ggttggcatc 300

ctctgggag tgatagcaat cttnttggcc accgttgtnn ntgaagtga 350

tgaagtgctt ggaagacgat gaggtgcaga agatgaggat ggctgtcatt 400

gggggcgcga tatttcttct tgcaggtctg gctatttttag ttgccacagc 450

atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccga 498

<210> 273

<211> 552

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394  
<223> unknown base

<400> 273

gggcccgacc attatccaac cgggntcact gttggctcat ctccctcctg 50  
gatgaancgc gccatcntca gactccctgc cccatggaga tttnnccat 100  
gctggcgaca acatcntgac cccagccat gtacgagggg ctttgaacgt 150  
cngcgtgtcg cagancaccg ggcagatcca gtgcaaagtc tttgactcct 200  
tgctgaatct gngcagcaca ttgcagcaac ccntgccctg atggtggttg 250  
gcatcctcct gggagtgata gcaatctttg tggccaccgt tggcatgaag 300  
tgtatgaagt gcttgaaga cgatgaggtg cagaagatga ggatggctgt 350  
cattgggggc gogatatttc ttcttgacagg tctggctatt tnnngttgcc 400  
acagcatggt atggcaatag aatcgttcaa gaattctatg accctatgac 450  
cccagtcaat gccaggtagc aatttggta ggctctcttc actggctggg 500  
ctgctgcttc tctctgcctt ctgggaggtg cctactttg ctgttcctgc 550  
ga 552

<210> 274

<211> 526

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407

<223> unknown base

<400> 274

attctccct cctggatgga tgcncacc gtcacattgc cttccccan 50  
tggaggattn actcctatgc tggcgacaac atcgtgaccc cccaggccat 100  
ttaccgaggg gctttggatg tcntgcntgt cgcagagcac cgggcagatc 150  
ccagtgcaaa gtctttgact ccttgctgaa tctgagcagc acattgcaag 200  
caaccctgac cttgatgggg ttggcatcct cctgggagtg atagcaacct 250  
ttgtggccac cggtggcatg aagtgtatga agtgcttgga agacgatgag 300  
gtgccagaag atgaggatgg ctgtcattgg gggcgcgata tttcttggtg 350  
caggctctggc tatttttagtn gccacagcat ggtatggcaa tagantnntt 400  
cnngnnntct atgaccctat gaccccagtc aatgccaggt acgaatttgg 450

tcaggctctc ttcactgggt gggctgctgc ttctctctgc cttctgggag 500  
gtgccctact ttgctgttcc tgtccc 526

<210> 275  
<211> 398  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274  
<223> unknown base

<400> 275  
agagcaccgg cagatcccag tncaaagtct ttgacccttg ctgaatctga 50  
gcagcacatt ncaagcaacc ccttgccttg aagggtggtg ncatcccccc 100  
tgggagtga tagcaatctt tgtggccacc gttggcatga agtntatgaa 150  
gtgcttgga gacgatgagg tgcagaagat gaggatggct gtcattgggg 200  
gcgcgatatt tcttcttgca ggtctggcta ttttagtnnc cacagcatgg 250  
tatggcaata gnatnnttcg nggnttctat gaccctatga cccagtcaa 300  
tgccaggtag gaatttggtc aggtctctct cactggctgg gctgctgctt 350  
ctctctgcct tctgggaggt gccctacttt gctgttcttg tccccgaa 398

<210> 276  
<211> 495  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476  
<223> unknown base

<400> 276  
agcaatgccc tgccccagt ggaggattaa ttcctatgnt ggggacaaca 50  
ttgtgacngc ccaggccatg tacggggggc tgtggatgct ctgcgtgtcg 100  
cagagcaccg ggcagatcca gtgcaaagtn tttgactcct tgctgaattt 150  
gagcagcaca ttgcaagcaa cccgtgcctt gatggtggtt ggcattctcc 200  
tgggagtgat agcaatcttt gtggccaccg tggnaatgaa gtgtatgaag 250  
tgcttggaag acgatgaggt gcagaagatg aggatggctg tcattggggg 300  
cgcgatatct cttnttgtag gtctggctat tttagttgcc acagcatggt 350  
atggcaatag aatngttcaa gaattttatg accctatgac cccagtcaat 400

gccaggtacg aatttgggtca ggctttnttc actggctggg ctgctgcttn 450

tttctgcctt ntgggaggtg ccctantttg ctgttcctgc gaacc 495

<210> 277

<211> 200

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 34, 87, 138, 147, 163, 165-166, 172

<223> unknown base

<400> 277

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cacagcatgg tatggcaata gaatcgttca agaattntat gaccctatga 100

ccccagtcaa tgccaggtac gaatttgggc aggctctntt cactggntgg 150

gctgctgctt ctntnngcct tntgggaggt gccctacttt gctgttctg 200

<210> 278

<211> 542

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 26, 43, 55, 77, 198, 361-362, 391-392, 396

<223> unknown base

<400> 278

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ttacncctat gctggcgaac aacatctga ccgccaggc catgtacgag 100

gggctgtgga atgtcctgcg tgtcccagag caccgggcag atccagtgc 150

aagtctttga ctcttgctg aatctgagca gcacattgca agcaaccntg 200

ccttgatggg ggttggcatc ctctgggag tgatagcaat ctttgtggcc 250

accgttggca tgaaagtgtg tgaagtgtt ggaagacgat gaggtgcaga 300

agatgaggat ggctgtcatt gggggcgaga tatttcttct tgcaggtctg 350

gctattttag nngccacagc atggatatggc aatcagaccc nntcanaaac 400

tctatgaccc tatgacccca gtcaatgcca ggtacgaatt tggtcaggct 450

ctcttcactg gctgggctgc tgcttctctc tgcttcttgg gaggtgcct 500

actttgctgt tcctgtcccc gaaaaacaac ctcttaccga cg 542

<210> 279  
<211> 548  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 90, 115, 147, 228, 387  
<223> unknown base

<400> 279  
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acaacatcgt gaccncccag gccatgtacg aggggctgtg gatgtcngcg 150  
tgtcgcacag caccgggcag atccagtgc aagtctttga ctccttgctg 200  
aatctgagca gcacattgca agcaacctg ccttgatggt ggttggcatc 250  
ctcctgggag tgatagcaat ctttgtggcc accgttggca tgaagtgtat 300  
gaagtgcttg gaagacgatg aggtgcagaa gatgaggatg gctgtcattg 350  
ggggcgcgat atttcttctt gcaggtctgg ctattntag ttgccacagc 400  
atggtatggc aatagaatcg ttcaagaatt ctatgacct atgaccccag 450  
tcaatgccag gtacgaattt ggtaggctc tcttactgg ctgggctgct 500  
gcttctctct gccttctggg aggtgcccta ctttgctgtt cctgcgaa 548

<210> 280  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 280  
cgagcgagtc atggccaacg c 21

<210> 281  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 281  
gtgtcacacg tagtctttcc cgctgg 26

<210> 282  
<211> 43



<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 282

ctgcagctgt tgggcttcat tctgccttc ctgggatgga tcg 43

<210> 283

<211> 2285

<212> DNA

<213> Homo sapiens

<400> 283

gcgtgccgtc agctcgccgg gcaccgaggc ctgccctcg cctccgccc 50  
ctgcgctgc accgcgtaga ccgaccccc cctccagcgc gccacccgg 100  
tagaggacc cgcggcgtag cccgaccggt cccgccttt ttgtaaaact 150  
taaagcgggc gcagcattaa cgcttccgc cccggtgacc tctcaggggt 200  
ctccccgcca aagggtgctc gccgctaagg aacatggcga aggtggagca 250  
ggtcctgagc ctgcagccgc agcacgagct caaattccga ggtcccttca 300  
ccgatgttgt caccaccaac cttaaagcttg gcaaccgac agaccgaaat 350  
gtgtgtttta aggtgaagac tacagcacca cgtaggtagt gtgtgaggcc 400  
caacagcggg atcatcgatg caggggcctc aattaatgta tctgtgatgt 450  
tacagccttt cgattatgat cccaatgaga aaagtaaaca caagtttatg 500  
gttcagtcta tgtttgcctc aactgacact tcagatatgg aagcagtatg 550  
gaaggaggca aaaccggaag accttatgga ttcaaaactt agatgtgtgt 600  
ttgaattgcc agcagagaat gataaaccac atgatgtaga aataaataaa 650  
attatatcca caactgcac aaagacagaa acaccaatag tgtctaagtc 700  
tctgagttct tctttggatg acaccgaagt taagaagggt atggaagaat 750  
gtaagaggct gcaaggtaga gttcagaggc tacgggagga gaacaagcag 800  
ttcaaggaag aagatggact gcggatgagg aagacagtgc agagcaacag 850  
ccccatttca gcattagccc caactgggaa ggaagaaggc cttagcacc 900  
ggctcttggc tctggtggtt ttgttcttta tcgttggtgt aattattggg 950  
aagattgcct tgtagaggta gcatgcacag gatggtaaat tggattggtg 1000  
gatccaccat atcatgggat ttaaatttat cataaccatg tgtaaaaaga 1050

aattaatgta tgatgacatc tcacaggtct tgcctttaaa ttaccctcc 1100  
ctgcacacac atacacagat acacacacac aaatataatg taacgatctt 1150  
ttagaaagtt aaaaatgtat agtaactgat tgagggggaa aaagaatgat 1200  
ctttattaat gacaaggaa accatgagta atgccacaat ggcatattgt 1250  
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tctcttaaaa tgacaccctt cctcgctgtg tgggtgctggc ccttggggag 1350  
ctggagccca gcatgctggg gagtgcggtc agtccacac agtagtccc 1400  
acgtggccca ctccggccc aggetgcttt ccgtgtcttc agttctgtcc 1450  
aagccatcag ctcttgga ctgatgaaca gagtcagaag cccaaaggaa 1500  
ttgcactgtg gcagcatcag acgtactcgt cataagtga aggctgtgt 1550  
tgactgattg acccagcgt ttggaaataa atggcagtgc tttgttact 1600  
taaaggacc aagctaaatt tgtattggt catgtagtga agtcaaactg 1650  
ttattcagag atgtttaatg catatttaac ttatttaatg tatttcact 1700  
catgttttct tattgtcaca agagtacagt taatgctgcg tgctgctgaa 1750  
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gcgagggcac cagcagttgt ggggtggggag caagggaaga gagaaactct 2150  
tcagcgaatc cttctagtag tagttgagag tttgactgtg aattaattt 2200  
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agaaaaatta taataaagcc ccaaaattaa gaaaa 2285

<210> 284

<211> 243

<212> PRT

<213> Homo sapiens

<400> 284

Met Ala Lys Val Glu Gln Val Leu Ser Leu Glu Pro Gln His Glu

1	5	10	15
Leu Lys Phe Arg Gly Pro Phe Thr Asp Val Val Thr Thr Asn Leu	20	25	30
Lys Leu Gly Asn Pro Thr Asp Arg Asn Val Cys Phe Lys Val Lys	35	40	45
Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly Ile	50	55	60
Ile Asp Ala Gly Ala Ser Ile Asn Val Ser Val Met Leu Gln Pro	65	70	75
Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val	80	85	90
Gln Ser Met Phe Ala Pro Thr Asp Thr Ser Asp Met Glu Ala Val	95	100	105
Trp Lys Glu Ala Lys Pro Glu Asp Leu Met Asp Ser Lys Leu Arg	110	115	120
Cys Val Phe Glu Leu Pro Ala Glu Asn Asp Lys Pro His Asp Val	125	130	135
Glu Ile Asn Lys Ile Ile Ser Thr Thr Ala Ser Lys Thr Glu Thr	140	145	150
Pro Ile Val Ser Lys Ser Leu Ser Ser Ser Leu Asp Asp Thr Glu	155	160	165
Val Lys Lys Val Met Glu Glu Cys Lys Arg Leu Gln Gly Glu Val	170	175	180
Gln Arg Leu Arg Glu Glu Asn Lys Gln Phe Lys Glu Glu Asp Gly	185	190	195
Leu Arg Met Arg Lys Thr Val Gln Ser Asn Ser Pro Ile Ser Ala	200	205	210
Leu Ala Pro Thr Gly Lys Glu Glu Gly Leu Ser Thr Arg Leu Leu	215	220	225
Ala Leu Val Val Leu Phe Phe Ile Val Gly Val Ile Ile Gly Lys	230	235	240

Ile Ala Leu

<210> 285

<211> 418

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 40, 53, 68, 119, 134, 177-178, 255  
<223> unknown base

<400> 285  
gtcagtcttc tagattgtcc ttatcccacc tttcaaccan tactcacatt 50  
tcnagcgccc aggtccangt ctgagcctga cttccccttg gggacctagc 100  
ctggagtcag gacaatggnt cgggctgcag aggnnttagaa gcgagggcac 150  
cagcagtttt ggggtggggag caagggngga gagaaactct tcagcgaatc 200  
cttctagtag tagttgagag ttgactgtg aattaatttt atgccataaa 250  
agacnaacc agttctgttt gactatgtag catcttgaaa agaaaaatta 300  
taataaagcc ccaaaattaa gaattctttt gtcattttgt cacatttgct 350  
ctatgggggg aattattatt ttatcatttt tattattttg ccattggaag 400  
gttaacttta aaatgagc 418

<210> 286  
<211> 543  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 73, 97  
<223> unknown base

<400> 286  
tattgtaaag gccattttaa accattggta ggccttggtg catgatgctg 50  
gattacctcc ttaaatgaca ccnttcctcg cctgttggtg ctggccnttg 100  
gggagctgga gccccagcat gctggggagt gcggtcagct ccacacagta 150  
gtccccacgt ggcccactcc cggcccaggc tgctttccgt gtcttcagtt 200  
ctgtccaagc catcagctcc ttgggactga tgaacagagt cagaagccca 250  
aaggaattgc cactgtggca gcatcagacg tactcgtcat aagtgagagg 300  
cgtgtgttga ctgattgacc cagcgctttg gaaataaatg gcagtgcctt 350  
gttcacttaa agggaccaag cttaaattgta ttggttcatg tagtgaagtc 400  
aaactgttat tcagagatgt ttaatgcata tttaacttat ttaatgtatt 450  
tcatctcatg ttttcttatt gtcacaagag tacagttaat gctgcgtgct 500  
gctgaactct gttgggtgaa ctggtattgc tgctggaggg ctg 543

<210> 287  
<211> 270

<212> DNA  
<213> Homo sapiens

<220>

<221> unsure

<222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242.

<223> unknown base

<400> 287

ccctggtggt tttgttcttt aattcgttgg tgtaattntt gggaagattg 50  
cttgttagagg tagnatgcac cnggctggta aattggattg gtggatccac 100  
catatccatg ggattttaaatt ttatcataac catgtgtaaa aagaaattaa 150  
tgtatgatga catntcacag gtattgcctt taaattaccc atccctgnan 200  
acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250  
agttaaaaat gtatagtaac 270

<210> 288

<211> 428

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 35, 116, 129, 197, 278, 294, 297, 349, 351

<223> unknown base

<400> 288

ggtggcccat tcccggccca ggctgctttc cggntttcag ttctgtccaa 50  
gccatcagct ccttgggact gatgaacaga gtcagaagcc caaaggaatt 100  
gcactgtggc agcatnagac gtacttgtna taagtgagag gcgtgtgttg 150  
actgattgac ccagcgcttt ggaaataaat ggcagtgcct tgttcantta 200  
aagggaacaa gctaaatttg tattgggttca tgtagtgaag tcaaactgtt 250  
attcagagat gtttaatgca tatttaantt atttaatgta ttnatntca 300  
tgttttctta ttgtcacaag agtacagtta atgctgcgtg ctgctgaant 350  
ntgttgggtg aactgggtatt gctgctggag ggctgtgggc tcctctgtct 400  
ttggagagtc tggatcatgtg gaggtggg 428

<210> 289

<211> 320

<212> DNA

<213> Homo sapiens

<400> 289

tgctttccgt gtcttcagtt ctgtccaagc catcagctcc ttgggaacttg 50

atgaacagag tcagaagccc aaaggaattg cactgtggca gcatcagacg 100  
tactcgtcat aagtgaagagg cgtgtgttga ctgattgacc cagcgctttg 150  
gaaataaatg gcagtgcctt gttcacttaa agggaccaag ctaaatttgt 200  
attggttcat gtagtgaagt caaactgtta ttcagagatg tttaatgcat 250  
atttaactta tttaatgtat ttcattctcat gttttcttat tgtcacaaga 300  
gtacagttaa tgctgcgtgc 320

<210> 290

<211> 609

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,  
447, 481, 513, 532, 584, 598

<223> unknown base

<400> 290

aaacctttaa aagttgaggg gaaaagaatg atcctttatt aatgacaagg 50  
gaaaccntgn gtaatccac aatggcatat tgtaaatgtc attttaaaca 100  
ttggtaggcc ttggtacatg atgctggatt acctctctta aaatgacacc 150  
cttcctcgcc tgttggtgct ggcccttggg gagctngagc ccagcatgct 200  
ggggagtgcg gtctgctcca cacagtagtc cccangtggc ccantcccgg 250  
cccaggctgc tttccgtgct ttcagttctg tccaagccat cagctccttg 300  
ggantgatga acagagtcag aagcccaaag gaattgcant gtggcagcat 350  
canganfant ngtcataagt gagaggcgtg tgttgantga ttgaccacgc 400  
gctttggaaa taaatggcag tgctttgttc anttaaaggg nccaagntaa 450  
atgtgtattg gttcatgtag tgaagtcaaa ntgttattca gagatgttta 500  
atgcatattt aanttattta atgtatttca tntcatgttt tcttattgtc 550  
acaagggtac agttaatgct gcgtgctgct gaantctgtt ggggtgaantg 600  
gtattgctg 609

<210> 291

<211> 493

<212> DNA

<213> Homo sapiens

<400> 291

ggcccttggg gagctggagc ccagcatgct ggggagtgcg gtcagctcca 50  
cacagtagtc cccacgtggc cactcccgg cccaggctgc tttccgtgtc 100  
ttcagttctg tccaagccat cagctccttg ggactgatga acagagtcag 150  
aagcccaaag gaattgcact gtggcagcat cagacgtact cgtcataagt 200  
gagaggcgtg tgttgactga ttgaccagc gctttggaaa taaatggcag 250  
tgctttgttc acttaaagg accaagctaa atttgtattg gttcatgtag 300  
tgaagtcaaa ctgttattca gagatgttta atgcatattt aacttattta 350  
atgtatttca tctcatgttt tcttattgtc acaagagtac agttaatgct 400  
gcgtgctgct gaactctgtt gggagaactg gtattgctgc tggagggctg 450  
tgggctcctc tgtctctgga gagtctggc atgtggaggt ggg 493

<210> 292

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 292

gcaccaccgt aggtacttgt gtgaggc 27

<210> 293

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

aaccaccaga gccaaagacc ggg 23

<210> 294

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cagcggaatc atcgatgcag gggcctcaat taatgtatct gtgatgttac 50

<210> 295

<211> 2530

<212> DNA

<213> Homo sapiens

<400> 295

gcgagctccg ggtgctgtgg cccggccttg gcggggcggc ctccgggtca 50  
ggctgggtga gaggtccca gctgcagcgt cccgcccgc ctccctcgga 100  
gctctgatct cagctgacag tgccctcggg gaccaaaca gcctggcagg 150  
gtctcacttt gttgcccagg ctggagttca gtgccatgat catggtttac 200  
tgcagccttg acctcctggg ttcaagcgat cctgctgagt agctgggact 250  
acaggacaaa attagaagat caaaatggaa aatatgctgc tttggttgat 300  
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attttatgtg gcacttgaga aaggtacccc ggattgtcag tgaaaggact 400  
ttccatctca ccagccccgc atttgaggca gatgctaaga tgatggtaaa 450  
tacagtgtgt ggcacgaat gccagaaaga actcccaact ccagccttt 500  
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 aatgtgaaat tgcatagata aaggtagatg gttaaagcaat tagtatcaga 1950  
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 cctaaaaatg aataaaattt atgaatatga 2530

<210> 296

<211> 413

<212> PRT

<213> Homo sapiens

<400> 296

Met	Glu	Asn	Met	Leu	Leu	Trp	Leu	Ile	Phe	Phe	Thr	Pro	Gly	Trp
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Thr Leu Ile Asp Gly Ser Glu Met Glu Trp Asp Phe Met Trp His

20	25	30
Leu Arg Lys Val Pro Arg Ile Val Ser Glu Arg Thr Phe His Leu		
35	40	45
Thr Ser Pro Ala Phe Glu Ala Asp Ala Lys Met Met Val Asn Thr		
50	55	60
Val Cys Gly Ile Glu Cys Gln Lys Glu Leu Pro Thr Pro Ser Leu		
65	70	75
Ser Glu Leu Glu Asp Tyr Leu Ser Tyr Glu Thr Val Phe Glu Asn		
80	85	90
Gly Thr Arg Thr Leu Thr Arg Val Lys Val Gln Asp Leu Val Leu		
95	100	105
Glu Pro Thr Gln Asn Ile Thr Thr Lys Gly Val Ser Val Arg Arg		
110	115	120
Lys Arg Gln Val Tyr Gly Thr Asp Ser Arg Phe Ser Ile Leu Asp		
125	130	135
Lys Arg Phe Leu Thr Asn Phe Pro Phe Ser Thr Ala Val Lys Leu		
140	145	150
Ser Thr Gly Cys Ser Gly Ile Leu Ile Ser Pro Gln His Val Leu		
155	160	165
Thr Ala Ala His Cys Val His Asp Gly Lys Asp Tyr Val Lys Gly		
170	175	180
Ser Lys Lys Leu Arg Val Gly Leu Leu Lys Met Arg Asn Lys Ser		
185	190	195
Gly Gly Lys Lys Arg Arg Gly Ser Lys Arg Ser Arg Arg Glu Ala		
200	205	210
Ser Gly Gly Asp Gln Arg Glu Gly Thr Arg Glu His Leu Gln Glu		
215	220	225
Arg Ala Lys Gly Gly Arg Arg Arg Lys Lys Ser Gly Arg Gly Gln		
230	235	240
Arg Ile Ala Glu Gly Arg Pro Ser Phe Gln Trp Thr Arg Val Lys		
245	250	255
Asn Thr His Ile Pro Lys Gly Trp Ala Arg Gly Gly Met Gly Asp		
260	265	270
Ala Thr Leu Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Arg Ala		
275	280	285
His Lys Lys Lys Tyr Met Glu Leu Gly Ile Ser Pro Thr Ile Lys		
290	295	300
Lys Met Pro Gly Gly Met Ile His Phe Ser Gly Phe Asp Asn Asp		

305	310	315
Arg Ala Asp Gln Leu Val Tyr Arg Phe Cys Ser Val Ser Asp Glu		
320	325	330
Ser Asn Asp Leu Leu Tyr Gln Tyr Cys Asp Ala Glu Ser Gly Ser		
335	340	345
Thr Gly Ser Gly Val Tyr Leu Arg Leu Lys Asp Pro Asp Lys Lys		
350	355	360
Asn Trp Lys Arg Lys Ile Ile Ala Val Tyr Ser Gly His Gln Trp		
365	370	375
Val Asp Val His Gly Val Gln Lys Asp Tyr Asn Val Ala Val Arg		
380	385	390
Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Leu Trp Ile His Gly		
395	400	405
Asn Asp Ala Asn Cys Ala Tyr Gly		
410		

<210> 297  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 297  
 gcatctgcag gagagagcga aggg 24

<210> 298  
 <211> 24  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 298  
 catcggtccc gtgaatccag aggc 24

<210> 299  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 299  
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<210> 300

<211> 1869

<212> DNA

<213> Homo sapiens

<400> 300

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tgtccgattc tgattccggc aaggatccaa gcatggaatg ctgccgtcgg 150  
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<210> 301

<211> 525

<212> PRT

<213> Homo sapiens

<400> 301

Met	Glu	Cys	Cys	Arg	Arg	Ala	Thr	Pro	Gly	Thr	Leu	Leu	Leu	Phe	1	5	10	15
Leu	Ala	Phe	Leu	Leu	Leu	Ser	Ser	Arg	Thr	Ala	Arg	Ser	Glu	Glu	20	25	30	
Asp	Arg	Asp	Gly	Leu	Trp	Asp	Ala	Trp	Gly	Pro	Trp	Ser	Glu	Cys	35	40	45	
Ser	Arg	Thr	Cys	Gly	Gly	Gly	Ala	Ser	Tyr	Ser	Leu	Arg	Arg	Cys	50	55	60	
Leu	Ser	Ser	Lys	Ser	Cys	Glu	Gly	Arg	Asn	Ile	Arg	Tyr	Arg	Thr	65	70	75	
Cys	Ser	Asn	Val	Asp	Cys	Pro	Pro	Glu	Ala	Gly	Asp	Phe	Arg	Ala	80	85	90	
Gln	Gln	Cys	Ser	Ala	His	Asn	Asp	Val	Lys	His	His	Gly	Gln	Phe	95	100	105	
Tyr	Glu	Trp	Leu	Pro	Val	Ser	Asn	Asp	Pro	Asp	Asn	Pro	Cys	Ser	110	115	120	
Leu	Lys	Cys	Gln	Ala	Lys	Gly	Thr	Thr	Leu	Val	Val	Glu	Leu	Ala	125	130	135	

Pro Lys Val Leu Asp Gly Thr Arg Cys Tyr Thr Glu Ser Leu Asp	140	145	150
Met Cys Ile Ser Gly Leu Cys Gln Ile Val Gly Cys Asp His Gln	155	160	165
Leu Gly Ser Thr Val Lys Glu Asp Asn Cys Gly Val Cys Asn Gly	170	175	180
Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr Lys Ser Gln	185	190	195
Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala Leu Pro Tyr	200	205	210
Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp His Leu	215	220	225
Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser	230	235	240
Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp	245	250	255
Phe Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro	260	265	270
Leu Thr Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala	275	280	285
Asp Ser Thr Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg	290	295	300
Trp Arg Glu Thr Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly	305	310	315
Gly Tyr Gln Leu Thr Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn	320	325	330
Arg Val Val Ala Asp Gln Tyr Cys His Tyr Tyr Pro Glu Asn Ile	335	340	345
Lys Pro Lys Pro Lys Leu Gln Glu Cys Asn Leu Asp Pro Cys Pro	350	355	360
Ala Ser Asp Gly Tyr Lys Gln Ile Met Pro Tyr Asp Leu Tyr His	365	370	375
Pro Leu Pro Arg Trp Glu Ala Thr Pro Trp Thr Ala Cys Ser Ser	380	385	390
Ser Cys Gly Gly Gly Ile Gln Ser Arg Ala Val Ser Cys Val Glu	395	400	405
Glu Asp Ile Gln Gly His Val Thr Ser Val Glu Glu Trp Lys Cys	410	415	420

Met	Tyr	Thr	Pro	Lys	Met	Pro	Ile	Ala	Gln	Pro	Cys	Asn	Ile	Phe
				425					430					435
Asp	Cys	Pro	Lys	Trp	Leu	Ala	Gln	Glu	Trp	Ser	Pro	Cys	Thr	Val
				440					445					450
Thr	Cys	Gly	Gln	Gly	Leu	Arg	Tyr	Arg	Val	Val	Leu	Cys	Ile	Asp
				455					460					465
His	Arg	Gly	Met	His	Thr	Gly	Gly	Cys	Ser	Pro	Lys	Thr	Lys	Pro
				470					475					480
His	Ile	Lys	Glu	Glu	Cys	Ile	Val	Pro	Thr	Pro	Cys	Tyr	Lys	Pro
				485					490					495
Lys	Glu	Lys	Leu	Pro	Val	Glu	Ala	Lys	Leu	Pro	Trp	Phe	Lys	Gln
				500					505					510
Ala	Gln	Glu	Leu	Glu	Glu	Gly	Ala	Ala	Val	Ser	Glu	Glu	Pro	Ser
				515					520					525

<210> 302  
 <211> 1533  
 <212> DNA  
 <213> Homo sapiens

<400> 302  
 cggacgcgtg ggcggcggct gcggaactcc cgtggagggg ccggtgggcc 50  
 ctcgggcctg acagatggca gtggccactg cggcggcagt actggccgct 100  
 ctgggcgggg cgctgtggct ggcggcccgc cggttcgtgg ggcccagggt 150  
 ccagcggctg cgcagaggcg gggaccccgg cctcatgcac gggaagactg 200  
 tgctgatcac cggggcgaaac agcggcctgg gccgcgccac ggccgcccag 250  
 ctactgcgcc tgggagcgcg ggtgatcatg ggctgccggg accgcgcgcg 300  
 cgccgaggag gcggcgggtc agctccgccg cgagctccgc caggccgcgg 350  
 agtgcgccc agagcctggc gtcagcggg tgggcgagct catagtccgg 400  
 gagctggacc tcgcctcgct gcgctcggtg cgcgccttct gccaggaaat 450  
 gctccaggaa gaggctaggc tggatgtctt gatcaataac gcagggatct 500  
 tccagtcccc ttacatgaag actgaagatg ggtttgagat gcagttcgga 550  
 gtgaaccatc tggggcactt tctactcacc aatcttctcc ttggactcct 600  
 caaaagtcca gctcccagca ggattgtggt agtttcttcc aaactttata 650  
 aatacggaga catcaatttt gatgacttga acagtgaaca aagctataat 700  
 aaaagctttt gttatagccg gagcaaactg gctaacattc tttttaccag 750

ggaactagcc cgccgcttag aaggcacaaa tgtcaccgtc aatgtgttgc 800  
 atcctggtat tgtacggaca aatctgggga ggcacataca cattccactg 850  
 ttggtcaaac cactcttcaa tttggtgtca tgggcttttt tcaaaactcc 900  
 agtagaaggt gccagactt ccatttatit ggcctcttca cctgaggtag 950  
 aaggagtgtc aggaagatac tttggggatt gtaaagagga agaactgttg 1000  
 cccaaagcta tggatgaatc tgttgcaaga aaactctggg atatcagtga 1050  
 agtgatggtt ggcctgctaa aataggaaca aggagtataa gagctgttta 1100  
 taaaactgca tatcagttat atctgtgatc aggaatggtg tggattgaga 1150  
 acttgttact tgaagaaaaa gaattttgat attggaatag cctgctaaga 1200  
 ggtacatgtg ggtattttgg agttactgaa aaattatttt tgggataaga 1250  
 gaatttcagc aaagatgttt taaatatata tagtaagtat aatgaataat 1300  
 aagtacaatg aaaaatacaa ttatattgta aaattataac tgggcaagca 1350  
 tggatgacat attaataatt gtcagaatta agtgactcaa agtgctatcg 1400  
 agaggttttt caagtatctt tgagtttcat ggccaaagtg ttaactagtt 1450  
 ttactacaat gtttggtggt tgtgtggaaa ttatctgcct ggtgtgtgca 1500  
 cacaagtctt acttgaata aatttactgg tac 1533

<210> 303

<211> 336

<212> PRT

<213> Homo sapiens

<400> 303

Met	Ala	Val	Ala	Thr	Ala	Ala	Ala	Val	Leu	Ala	Ala	Leu	Gly	Gly
1				5				10					15	

Ala	Leu	Trp	Leu	Ala	Ala	Arg	Arg	Phe	Val	Gly	Pro	Arg	Val	Gln
			20					25						30

Arg	Leu	Arg	Arg	Gly	Gly	Asp	Pro	Gly	Leu	Met	His	Gly	Lys	Thr
				35				40						45

Val	Leu	Ile	Thr	Gly	Ala	Asn	Ser	Gly	Leu	Gly	Arg	Ala	Thr	Ala
				50				55						60

Ala	Glu	Leu	Leu	Arg	Leu	Gly	Ala	Arg	Val	Ile	Met	Gly	Cys	Arg
				65				70						75

Asp	Arg	Ala	Arg	Ala	Glu	Glu	Ala	Ala	Gly	Gln	Leu	Arg	Arg	Glu
				80				85						90

Leu	Arg	Gln	Ala	Ala	Glu	Cys	Gly	Pro	Glu	Pro	Gly	Val	Ser	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



95	100	105
Val Gly Glu Leu Ile Val Arg Glu Leu Asp Leu Ala Ser Leu Arg		
110	115	120
Ser Val Arg Ala Phe Cys Gln Glu Met Leu Gln Glu Glu Pro Arg		
125	130	135
Leu Asp Val Leu Ile Asn Asn Ala Gly Ile Phe Gln Cys Pro Tyr		
140	145	150
Met Lys Thr Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His		
155	160	165
Leu Gly His Phe Leu Leu Thr Asn Leu Leu Leu Gly Leu Leu Lys		
170	175	180
Ser Ser Ala Pro Ser Arg Ile Val Val Val Ser Ser Lys Leu Tyr		
185	190	195
Lys Tyr Gly Asp Ile Asn Phe Asp Asp Leu Asn Ser Glu Gln Ser		
200	205	210
Tyr Asn Lys Ser Phe Cys Tyr Ser Arg Ser Lys Leu Ala Asn Ile		
215	220	225
Leu Phe Thr Arg Glu Leu Ala Arg Arg Leu Glu Gly Thr Asn Val		
230	235	240
Thr Val Asn Val Leu His Pro Gly Ile Val Arg Thr Asn Leu Gly		
245	250	255
Arg His Ile His Ile Pro Leu Leu Val Lys Pro Leu Phe Asn Leu		
260	265	270
Val Ser Trp Ala Phe Phe Lys Thr Pro Val Glu Gly Ala Gln Thr		
275	280	285
Ser Ile Tyr Leu Ala Ser Ser Pro Glu Val Glu Gly Val Ser Gly		
290	295	300
Arg Tyr Phe Gly Asp Cys Lys Glu Glu Glu Leu Leu Pro Lys Ala		
305	310	315
Met Asp Glu Ser Val Ala Arg Lys Leu Trp Asp Ile Ser Glu Val		
320	325	330
Met Val Gly Leu Leu Lys		
335		

<210> 304

<211> 521

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 20, 34, 62, 87, 221, 229

<223> unknown base

<400> 304

ggggattgta aagaggaagn actgtgccca aagntatgga tgaatctgtt 50  
gcaagaaaat tntgggatat cagtgaagtg atggttngcc tgctaaaata 100  
ggaacaagga gtaaaagagc tgtttataaa actgcatatc agttatatct 150  
gtgatcagga atggtgtgga ttgagaactt gttacttgaa gaaaaagaat 200  
tttgatattg gaatagcctg ntaagaggna catgtgggta ttttgagtt 250  
actgaaaaat ttttttggg ataagagaat ttcagcaaag atgtttttaa 300  
tatatatagt aagtataatg aataataagt acaatgaaaa atacaattat 350  
attgtaaaat tataactggg caagcatgga tgacatatta atatttgtca 400  
gaattaagtg actcaaagtg ctatcgagag gtttttcaag tatctttgag 450  
tttcatggcc aaagtgttaa ctagttttac tacaatgttt ggtgtttgtg 500  
tggaattat ctgcctggct t 521

<210> 305

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 305

ccaggaaatg ctccaggaag agcc 24

<210> 306

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 306

gcccatgaca ccaaattgaa gagtgg 26

<210> 307

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 307

aacgcagga tcttccagtg cccttacatg aagactgaag atggg 45

<210> 308

<211> 1523

<212> DNA

<213> Homo sapiens

<400> 308

gagaggacga ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 50  
cggagcccag ccctttccta acccaaccca acctagccca gtcccagccg 100  
ccagcgcctg tccctgtcac ggaccccagc gttaccatgc atcctgccgt 150  
cttcctatcc ttacccgacc tcagatgctc ctttctgctc ctggtaactt 200  
gggtttttac tcctgtaaca actgaaataa caagtcttgc tacagagaat 250  
atagatgaaa ttttaaacaa tgctgatgtt gctttagtaa atttttatgc 300  
tgactggtgt cgtttcagtc agatgttgca tccaattttt gaggaagctt 350  
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 400  
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 450  
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 500  
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggcaa 550  
caaaaaagtg accccattca agaaattcgg gacttagcag aaatcaccac 600  
tcttgatcgc agcaaaagaa atatcattgg atattttgag caaaaggact 650  
cggacaacta tagagttttt gaacgagtag cgaatatattt gcatgatgac 700  
tgtgcctttc tttctgcatt tggggatgtt tcaaaaccgg aaagatatag 750  
tggcgacaac ataatctaca aaccaccagg gcattctgct ccggatatgg 800  
tgtacttggg agctatgaca aattttgatg tgacttacia ttggattcaa 850  
gataaatgtg ttcctcttgt ccgagaaata acatttgaaa atggagagga 900  
attgacagaa gaaggactgc cttttctcat actctttcac atgaaagaag 950  
atacagaaag tttagaaata ttccagaatg aagtagctcg gcaattaata 1000  
agtgaaaaag gtacaataaa ctttttacat gccgattgtg acaaatttag 1050  
acatcctctt ctgcacatac agaaaactcc agcagattgt cctgtaatcg 1100  
ctattgacag ctttaggcat atgtatgtgt ttggagactt caaagatgta 1150  
ttaattcctg gaaaactcaa gcaattcgta tttgacttac attctggaaa 1200  
actgcacaga gaattccatc atggacctga cccaactgat acagccccag 1250

gagagcaagc ccaagatgta gcaagcagtc cacctgagag ctccttccag 1300  
 aaactagcac ccagtgaata taggtatact ctattgaggg atcgagatga 1350  
 gcttttaaaaa cttgaaaaac agtttgtaag cctttcaaca gcagcatcaa 1400  
 cctacgtggg ggaaatagta aacctatatt ttcataattc tatgtgtatt 1450  
 tttatttttga ataaacagaa agaaatttaa aaaaaaaaaa aaaaaaaaaa 1500  
 aaaaaaaaaa aaaaaaaaaa aaa 1523

<210> 309  
 <211> 406  
 <212> PRT  
 <213> Homo sapiens

<400> 309  
 Met His Pro Ala Val Phe Leu Ser Leu Pro Asp Leu Arg Cys Ser  
 1 5 10 15  
 Leu Leu Leu Leu Val Thr Trp Val Phe Thr Pro Val Thr Thr Glu  
 20 25 30  
 Ile Thr Ser Leu Ala Thr Glu Asn Ile Asp Glu Ile Leu Asn Asn  
 35 40 45  
 Ala Asp Val Ala Leu Val Asn Phe Tyr Ala Asp Trp Cys Arg Phe  
 50 55 60  
 Ser Gln Met Leu His Pro Ile Phe Glu Glu Ala Ser Asp Val Ile  
 65 70 75  
 Lys Glu Glu Phe Pro Asn Glu Asn Gln Val Val Phe Ala Arg Val  
 80 85 90  
 Asp Cys Asp Gln His Ser Asp Ile Ala Gln Arg Tyr Arg Ile Ser  
 95 100 105  
 Lys Tyr Pro Thr Leu Lys Leu Phe Arg Asn Gly Met Met Met Lys  
 110 115 120  
 Arg Glu Tyr Arg Gly Gln Arg Ser Val Lys Ala Leu Ala Asp Tyr  
 125 130 135  
 Ile Arg Gln Gln Lys Ser Asp Pro Ile Gln Glu Ile Arg Asp Leu  
 140 145 150  
 Ala Glu Ile Thr Thr Leu Asp Arg Ser Lys Arg Asn Ile Ile Gly  
 155 160 165  
 Tyr Phe Glu Gln Lys Asp Ser Asp Asn Tyr Arg Val Phe Glu Arg  
 170 175 180  
 Val Ala Asn Ile Leu His Asp Asp Cys Ala Phe Leu Ser Ala Phe  
 185 190 195

Gly Asp Val Ser Lys Pro Glu Arg Tyr Ser Gly Asp Asn Ile Ile	200	205	210
Tyr Lys Pro Pro Gly His Ser Ala Pro Asp Met Val Tyr Leu Gly	215	220	225
Ala Met Thr Asn Phe Asp Val Thr Tyr Asn Trp Ile Gln Asp Lys	230	235	240
Cys Val Pro Leu Val Arg Glu Ile Thr Phe Glu Asn Gly Glu Glu	245	250	255
Leu Thr Glu Glu Gly Leu Pro Phe Leu Ile Leu Phe His Met Lys	260	265	270
Glu Asp Thr Glu Ser Leu Glu Ile Phe Gln Asn Glu Val Ala Arg	275	280	285
Gln Leu Ile Ser Glu Lys Gly Thr Ile Asn Phe Leu His Ala Asp	290	295	300
Cys Asp Lys Phe Arg His Pro Leu Leu His Ile Gln Lys Thr Pro	305	310	315
Ala Asp Cys Pro Val Ile Ala Ile Asp Ser Phe Arg His Met Tyr	320	325	330
Val Phe Gly Asp Phe Lys Asp Val Leu Ile Pro Gly Lys Leu Lys	335	340	345
Gln Phe Val Phe Asp Leu His Ser Gly Lys Leu His Arg Glu Phe	350	355	360
His His Gly Pro Asp Pro Thr Asp Thr Ala Pro Gly Glu Gln Ala	365	370	375
Gln Asp Val Ala Ser Ser Pro Pro Glu Ser Ser Phe Gln Lys Leu	380	385	390
Ala Pro Ser Glu Tyr Arg Tyr Thr Leu Leu Arg Asp Arg Asp Glu	395	400	405

Leu

<210> 310  
 <211> 182  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 36, 48  
 <223> unknown base

<400> 310

attaaggaag aatttccaaa tgaaaatcaa gtagtntttg ccagagtnga 50  
ttgtgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100  
caaccctcaa attgtttcgt aatgggatga tgatgaagag agaatacagg 150  
ggtcagcgat cagtgaaagc attggcagat ta 182

<210> 311

<211> 598

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396

<223> unknown base

<400> 311

agaggcctct ctggaagttg tcccgggtgt tcgccgcngg agcccgggtc 50  
gagaggacna ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 100  
cggagcccag ccctttccta acccaaccca acctagcccn gtcccagccg 150  
ccagcgcctg tccctgtcnc ggancccagc gtnaccatgc atcctgccgt 200  
cttcctatcc ttacccgacc tcagatgctc ccttctgctc ctggtaactt 250  
gggttttttac tctgttaaca actgaaataa cnngtcttga tacnnagaat 300  
atagatgaaa ttttaaacna tgctgatgtg gctttagtca atttttatgc 350  
tgactgggtg cgtttcagtc agatgtggca tccaattttt gaggangctt 400  
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 450  
agagttgatt gtgatcagca ctctgacata gcccagagat acaggataag 500  
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 550  
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggc 598

<210> 312

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 312

tgagaggcct ctctggaagt tg 22

<210> 313

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 313

gtcagcgatc agtgaaagc 19

<210> 314

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 314

ccagaatgaa gtagctcggc 20

<210> 315

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 315

ccgactcaaa atgcattgtc 20

<210> 316

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 316

catttggcag gaattgtcc 19

<210> 317

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 317

ggtgctatag gccaaagg 18

<210> 318

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 318

ctgtatctct gggctatgtc agag 24

<210> 319

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 319

ctacatataa tggcacatgt cagcc 25

<210> 320

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 320

cgtcttccta tccttaccgc acctcagatg ctcccttctg ctctg 46

<210> 321

<211> 1333

<212> DNA

<213> Homo sapiens

<400> 321

gcccacgcgt ccgatggcgt tcacgttcgc ggcccttctgc tacatgctgg 50

cgctgctgct cactgccgcg ctcatcttct tcgccatttg gcacattata 100

gcatttgatg agctgaagac tgattacaag aatcctatag accagtgtaa 150

taccctgaat ccccttgtag tcccagagta cctcatccac gctttcttct 200

gtgtcatggt tctttgtgca gcagagtggc ttacactggg tctcaatatg 250

cccccttgg catatcatat ttggaggtat atgagtagac cagtgatgag 300

tggcccagga ctctatgacc ctacaaccat catgaatgca gatattctag 350

catattgtca gaaggaagga tgggtgcaaat tagcttttta tcttctagca 400

tttttttact acctatatgg catgatctat gttttggtga gctcttagaa 450

caacacacag aagaattggt ccagttaagt gcatgcaaaa agccaccaa 500

tgaagggatt ctatccagca agatcctgtc caagagtagc ctgtggaatc 550

tgatcagtta ctttaaaaaa tgactcctta ttttttaaata gtttccacat 600



ttttgcttgt ggaaagactg ttttcatatg ttatactcag ataaagattt 650  
 taaatggtat tacgtataaa ttaatatata atgattacct ctggtgttga 700  
 caggtttgaa cttgcacttc ttaaggaaca gccataatcc tctgaatgat 750  
 gcattaatta ctgactgtcc tagtacattg gaagcttttg tttataggaa 800  
 cttgtagggc tcatttttgg ttcattgaaa cagtatctaa ttataaatta 850  
 gctgtagata tcaggtgctt ctgatgaagt gaaaatgtat atctgactag 900  
 tgggaaactt catgggtttc ctcatctgtc atgtcgatga ttatatatgg 950  
 atacatttac aaaaataaaa agcgggaatt ttcccttcgc ttgaatatta 1000  
 tccctgtata ttgcatgaat gagagatttc ccatatttcc atcagagtaa 1050  
 taaatatact tgctttaatt cttaagcata agtaaacaatg atataaaaat 1100  
 atatgctgaa ttacttgtga agaatgcatt taaagctatt ttaaatgtgt 1150  
 ttttatttgt aagacattac ttattaagaa attggttatt atgcttactg 1200  
 ttctaactctg gtggtaaagg tattcttaag aatttgcagg tactacagat 1250  
 tttcaaaact gaatgagaga aaattgtata accatcctgc tgttccttta 1300  
 gtgcaataca ataaaactct gaaattaaga ctc 1333

<210> 322

<211> 144

<212> PRT

<213> Homo sapiens

<400> 322

Met	Ala	Phe	Thr	Phe	Ala	Ala	Phe	Cys	Tyr	Met	Leu	Ala	Leu	Leu
1				5				10					15	
Leu	Thr	Ala	Ala	Leu	Ile	Phe	Phe	Ala	Ile	Trp	His	Ile	Ile	Ala
				20				25					30	
Phe	Asp	Glu	Leu	Lys	Thr	Asp	Tyr	Lys	Asn	Pro	Ile	Asp	Gln	Cys
				35				40					45	
Asn	Thr	Leu	Asn	Pro	Leu	Val	Leu	Pro	Glu	Tyr	Leu	Ile	His	Ala
				50				55					60	
Phe	Phe	Cys	Val	Met	Phe	Leu	Cys	Ala	Ala	Glu	Trp	Leu	Thr	Leu
				65				70					75	
Gly	Leu	Asn	Met	Pro	Leu	Leu	Ala	Tyr	His	Ile	Trp	Arg	Tyr	Met
				80				85					90	
Ser	Arg	Pro	Val	Met	Ser	Gly	Pro	Gly	Leu	Tyr	Asp	Pro	Thr	Thr
				95				100					105	

Ile Met Asn Ala Asp Ile Leu Ala Tyr Cys Gln Lys Glu Gly Trp  
110 115 120

Cys Lys Leu Ala Phe Tyr Leu Leu Ala Phe Phe Tyr Tyr Leu Tyr  
125 130 135

Gly Met Ile Tyr Val Leu Val Ser Ser  
140

<210> 323

<211> 477

<212> DNA

<213> Homo sapiens

<400> 323

attatagcat ttgatgagct gaagactgat tacaagatcc tatagaccag 50  
tgtaataccc tgaatcccct tgtactccca gactacctca tccacgcttt 100  
cttctgtgtc atgtttcttt gtgcagcaga gtggcttaca ctgggtctca 150  
atatgcccct cttggcatat catatttggg ggtatatgag tagaccagtg 200  
atgagtggcc caggactcta tgaccctaca accatcatga atgcagatat 250  
tctagcatat tgtcagaagg aaggatggtg caaattagct ttttatcttc 300  
tagcatTTTT ttactaccta tatggcatga tctatgtttt ggtgagctct 350  
tagaacaaca cacagaagaa ttggtccagt taagtgcatt caaaaagcca 400  
ccaaatgaag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450  
gaatctgatt agttacttta aaaaatg 477

<210> 324

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 324

tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 325

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 325

caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 326  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 326  
gtgcagcaga gtggcttaca 20

<210> 327  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 327  
actggaccaa ttcttctgtg 20

<210> 328  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 328  
gatattctag catattgtca gaaggaagga tggcgcaaat tagct 45

<210> 329  
<211> 1174  
<212> DNA  
<213> Homo sapiens

<400> 329  
cggacgcgtg ggggaaaccc ttccgagaaa acagcaacaa gctgagctgc 50  
tgtgacagag gggacaaga tggcggcgcc gaaggggagc ctctgggtga 100  
ggaccaact ggggtcccg ccgctgctgc tgctgaccat ggccttggcc 150  
ggagggttcgg ggaccgcttc ggctgaagca tttgactcgg tcttgggtga 200  
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accctaagga agaggagttg tacgcatgtc agagaggttg caggctgttt 300  
tcaatttgtc agtttgtgga tgatggaatt gacttaaata gaactaaatt 350  
ggaatgtgaa tctgcatgta cagaagcata ttcccaatct gatgagcaat 400  
atgcttgcca tcttggttgc cagaatcagc tgccattcgc tgaactgaga 450



Gln Ser Asp Glu Gln Tyr Ala Cys His Leu Gly Cys Gln Asn Gln	110	115	120
Leu Pro Phe Ala Glu Leu Arg Gln Glu Gln Leu Met Ser Leu Met	125	130	135
Pro Lys Met His Leu Leu Phe Pro Leu Thr Leu Val Arg Ser Phe	140	145	150
Trp Ser Asp Met Met Asp Ser Ala Gln Ser Phe Ile Thr Ser Ser	155	160	165
Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys Ile Val Ile Phe	170	175	180
Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu Glu Gln Glu	185	190	195
Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser Tyr Leu	200	205	210
Gln Met Arg Asn Ser Gln Ala His Arg Asn Phe Leu Glu Asp Gly	215	220	225
Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn Ser Gly Trp	230	235	240
Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu Leu Trp	245	250	255
Ile Cys Cys Ala Thr Val Ala Thr Ala Val Glu Gln Tyr Val Pro	260	265	270
Ser Glu Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe Met Asn Glu	275	280	285
Gln Lys Leu Asn Arg Tyr Pro Ala Ser Ser Leu Val Val Val Arg	290	295	300
Ser Lys Thr Glu Asp His Glu Glu Ala Gly Pro Leu Pro Thr Lys	305	310	315
Val Asn Leu Ala His Ser Glu Ile	320		

<210> 331

<211> 350

<212> DNA

<213> Homo sapiens

<400> 331

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gcacacctac cctaaggaag aggagttgta cgcattgtcag agaggttgca 100

ggctgttttc aatttgtcag tttgtggatg atggaattga cttaaatacga 150

actaaattgg aatgtgaatc tgcattgtaca gaagcatatt cccaatctga 200  
tgagcaatat gcttgccatc ttggttgcca gaatcagctg ccattcgctg 250  
aactgagaca agaacaactt atgtccctga tgccaaaaat gcacctactc 300  
tttcctctaa ctctgggtgag gtcattctgg agtgacatga tggactccgc 350

<210> 332  
<211> 562  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 47  
<223> unknown base

<400> 332  
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aaacagcaac aagctgagct gctgtgacag agggacaag atggcggcgc 100  
cgaagggagc ctttggtgga ggaccaact ggggctcccg ccgctgctgc 150  
tgctgaccat ggccttggcc ggagggttcgg ggaccgcttc ggctgaagca 200  
tttgactcgg tcttggtgga tacggcgtct tgccaccggg cctgtcagtt 250  
gacctacccc ttgcacacct accctaagga agaggagttg tacgcatgtc 300  
agagaggttg caggctgttt tcaatttgtc agtttggtga tgatggaatt 350  
gacttaaadc gaactaaatt ggaatgtgaa tctgcatgta cagaagcata 400  
ttcccaatct gatgagcaat atgcttgcca tcttggttgc cagaatcagc 450  
tgccattcgc tgaactgaga caagaacaac ttatgtccct gatgccaaaa 500  
atgcacctac tctttcctct aactctggtg aggtcattct ggagtgacat 550  
gatggactcc gc 562

<210> 333  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 333  
acaagctgag ctgctgtgac ag 22

<210> 334  
<211> 22

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 334  
tgattctggc aaccaagatg gc 22

<210> 335  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 335  
atggccttgg ccggagggttc ggggaccgct tcggctgaag 40

<210> 336  
<211> 1885  
<212> DNA  
<213> Homo sapiens

<400> 336  
gcgaggtggc gatcgctgag aggcaggagg gccgaggcgg gcctgggagg 50  
cgggccggag gtggggcgcc gctggggccg gcccgcacgg gttcatctg 100  
agggcgacg gcccgcgacc gagcgtgcgg actggcctcc caagcgtggg 150  
gcgacaagct gccggagctg caatgggccc cggctgggga ttcttgtttg 200  
gcctcctggg cgccgtgtgg ctgctcagct cgggccacgg agaggagcag 250  
cccccggaga cagcggcaca gaggtgcttc tgccagggtta gtggttactt 300  
ggatgattgt acctgtgatg ttgaaaccat tgatagattt aataactaca 350  
ggcttttccc aagactacaa aaacttcttg aaagtgacta ctttaggtat 400  
tacaaggtaa acctgaagag gccgtgtcct ttctggaatg acatcagcca 450  
gtgtggaaga agggactgtg ctgtcaaacc atgtcaatct gatgaagttc 500  
ctgatggaat taaatctgcg agctacaagt attctgaaga agccaataat 550  
ctcattgaag aatgtgaaca agctgaacga cttggagcag tggatgaatc 600  
tctgagttag gaaacacaga aggctgttct tcagtggacc aagcatgatg 650  
attcttcaga taacttctgt gaagctgatg acattcagtc ccctgaagct 700  
gaatatgtag atttgcttct taatcctgag cgctacactg gttacaaggg 750  
accagatgct tggaaaatat ggaatgtcat ctacgaagaa aactgtttta 800

agccacagac aattaaaga cctttaaatc ctttggcttc tgggtcaagg 850  
 acaagtgaag agaacacttt ttacagttgg ctagaaggtc tctgtgtaga 900  
 aaaaagagca ttctacagac ttatatctgg cctacatgca agcattaatg 950  
 tgcatttgag tgcaagatat cttttacaag agacctgggt agaaaagaaa 1000  
 tggggacaca acattacaga atttcaacag cgatttgatg gaattttgac 1050  
 tgaaggagaa ggtccaagaa ggcttaagaa cttgtatctt ctctacttaa 1100  
 tagaactaag ggctttatcc aaagtgttac cattcttcga gcgcccagat 1150  
 tttcaactct ttactggaaa taaaattcag gatgaggaaa acaaaatggt 1200  
 acttctggaa atacttcatg aaatcaagtc atttcctttg cattttgatg 1250  
 agaattcatt ttttgctggg gataaaaaag aagcacacaa actaaaggag 1300  
 gactttcgac tgcattttag aaatatttca agaattatgg attgtgttgg 1350  
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 attcaacgca ttggaagaa tttctacaag tgtgaaagaa ttagaaaact 1550  
 tcaggaactt gttacagaat attcattaaa gaaaacaagc tgatatgtgc 1600  
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 aaggagaatt atattgtttt aagtaaacac atttttaaaa attgtgttaa 1750  
 gtctatgtat aatactactg tgagtaaaag taatacttta ataatgtggt 1800  
 acaaatttta aagtttaata ttgaataaaa ggaggattat caaattaaaa 1850  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1885

<210> 337

<211> 468

<212> PRT

<213> Homo sapiens

<400> 337

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Trp	Leu	Leu	Ser	Ser	Gly	His	Gly	Glu	Glu	Gln	Pro	Pro	Glu	Thr
				20				25					30	



Ala	Ala	Gln	Arg	Cys	Phe	Cys	Gln	Val	Ser	Gly	Tyr	Leu	Asp	Asp	
				35					40					45	
Cys	Thr	Cys	Asp	Val	Glu	Thr	Ile	Asp	Arg	Phe	Asn	Asn	Tyr	Arg	
				50					55					60	
Leu	Phe	Pro	Arg	Leu	Gln	Lys	Leu	Leu	Glu	Ser	Asp	Tyr	Phe	Arg	
				65					70					75	
Tyr	Tyr	Lys	Val	Asn	Leu	Lys	Arg	Pro	Cys	Pro	Phe	Trp	Asn	Asp	
				80					85					90	
Ile	Ser	Gln	Cys	Gly	Arg	Arg	Asp	Cys	Ala	Val	Lys	Pro	Cys	Gln	
				95					100					105	
Ser	Asp	Glu	Val	Pro	Asp	Gly	Ile	Lys	Ser	Ala	Ser	Tyr	Lys	Tyr	
				110					115					120	
Ser	Glu	Glu	Ala	Asn	Asn	Leu	Ile	Glu	Glu	Cys	Glu	Gln	Ala	Glu	
				125					130					135	
Arg	Leu	Gly	Ala	Val	Asp	Glu	Ser	Leu	Ser	Glu	Glu	Thr	Gln	Lys	
				140					145					150	
Ala	Val	Leu	Gln	Trp	Thr	Lys	His	Asp	Asp	Ser	Ser	Asp	Asn	Phe	
				155					160					165	
Cys	Glu	Ala	Asp	Asp	Ile	Gln	Ser	Pro	Glu	Ala	Glu	Tyr	Val	Asp	
				170					175					180	
Leu	Leu	Leu	Asn	Pro	Glu	Arg	Tyr	Thr	Gly	Tyr	Lys	Gly	Pro	Asp	
				185					190					195	
Ala	Trp	Lys	Ile	Trp	Asn	Val	Ile	Tyr	Glu	Glu	Asn	Cys	Phe	Lys	
				200					205					210	
Pro	Gln	Thr	Ile	Lys	Arg	Pro	Leu	Asn	Pro	Leu	Ala	Ser	Gly	Gln	
				215					220					225	
Gly	Thr	Ser	Glu	Glu	Asn	Thr	Phe	Tyr	Ser	Trp	Leu	Glu	Gly	Leu	
				230					235					240	
Cys	Val	Glu	Lys	Arg	Ala	Phe	Tyr	Arg	Leu	Ile	Ser	Gly	Leu	His	
				245					250					255	
Ala	Ser	Ile	Asn	Val	His	Leu	Ser	Ala	Arg	Tyr	Leu	Leu	Gln	Glu	
				260					265					270	
Thr	Trp	Leu	Glu	Lys	Lys	Trp	Gly	His	Asn	Ile	Thr	Glu	Phe	Gln	
				275					280					285	
Gln	Arg	Phe	Asp	Gly	Ile	Leu	Thr	Glu	Gly	Glu	Gly	Pro	Arg	Arg	
				290					295					300	
Leu	Lys	Asn	Leu	Tyr	Phe	Leu	Tyr	Leu	Ile	Glu	Leu	Arg	Ala	Leu	
				305					310					315	

Ser Lys Val Leu Pro Phe Phe Glu Arg Pro Asp Phe Gln Leu Phe  
 320 325 330  
 Thr Gly Asn Lys Ile Gln Asp Glu Glu Asn Lys Met Leu Leu Leu  
 335 340 345  
 Glu Ile Leu His Glu Ile Lys Ser Phe Pro Leu His Phe Asp Glu  
 350 355 360  
 Asn Ser Phe Phe Ala Gly Asp Lys Lys Glu Ala His Lys Leu Lys  
 365 370 375  
 Glu Asp Phe Arg Leu His Phe Arg Asn Ile Ser Arg Ile Met Asp  
 380 385 390  
 Cys Val Gly Cys Phe Lys Cys Arg Leu Trp Gly Lys Leu Gln Thr  
 395 400 405  
 Gln Gly Leu Gly Thr Ala Leu Lys Ile Leu Phe Ser Glu Lys Leu  
 410 415 420  
 Ile Ala Asn Met Pro Glu Ser Gly Pro Ser Tyr Glu Phe His Leu  
 425 430 435  
 Thr Arg Gln Glu Ile Val Ser Leu Phe Asn Ala Phe Gly Arg Ile  
 440 445 450  
 Ser Thr Ser Val Lys Glu Leu Glu Asn Phe Arg Asn Leu Leu Gln  
 455 460 465

Asn Ile His

<210> 338

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 101, 263, 376, 397, 426

<223> unknown base

<400> 338

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 nacacttttt acagttggct agaaggtctc tgtgtagaaa aaagagcatt 150  
 ctacagactt atatctggcc tacatgcaag cattaatgtg catttgagtg 200  
 caagatatct tttaacaagag acctgggttag aaaagaaatg gggacacaac 250  
 attacagaat ttnaacagcg atttgatgga attttgactg aaggagaagg 300  
 tccaagaagg cttaagaact tgtattttct ctacttaata gaactaaggg 350

ctttatccaa agtggttacca ttcttngagc gcccagattt tcaactnttt 400  
actggaaata aaattcagga tgaggnaaac aaaatgttac ttttggaat 450  
acttcatgaa atcaagtcac ttcccttgca ttttgatgag aattcatttt 500  
tttgctg 507

<210> 339  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 339  
aagctgccgg agctgcaatg 20

<210> 340  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 340  
ttgcttctta atcctgagcg c 21

<210> 341  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 341  
aaaggaggac tttcgactgc 20

<210> 342  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 342  
agagattcat ccaactgctcc aagtcg 26

<210> 343  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 343

tgtccagaaa caggcacata tcagc 25

<210> 344

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

agacagcggc acagaggtgc ttctgccagg ttagtggtta cttggatgat 50

<210> 345

<211> 1486

<212> DNA

<213> Homo sapiens

<400> 345

cggacgcgtg ggcggacgcg tgggcggacg cgtgggttgg gagggggcag 50

gatgggaggg aaagtgaaga aaacagaaaa ggagagggac agaggccaga 100

ggactttctca tactggacag aaaccgatca ggcattggaac tccccttcgt 150

cactcacctg ttcttgcccc tgggtgttct gacaggtctc tgctccccct 200

ttaacctgga tgaacatcac ccacgcctat tcccagggcc accagaagct 250

gaatttgat acagtgtctt acaacatgtt gggggtggac agcgatgat 300

gctggtgggc gccccctggg atgggccttc aggcgaccgg aggggggacg 350

tttatcgctg ccctgtaggg ggggccaca atgccccatg tgccaagggc 400

cacttaggtg actaccaact gggaaattca tctcatctg ctgtgaatat 450

gcacctgggg atgtctctgt tagagacaga tggatgatgg ggattcatgg 500

tgagctaagg agaggggtgtt ggcagtgtct ctgaaggctc ataaaagaaa 550

aaagagaagt gtggttaagg aaaatggtct gtgtggagg gtcaaggagt 600

taaaaaccct agaaagcaaa aggtaggtta tgtcaggag tagtcttcat 650

gcctccttca actgggagca tgttctgagg gtgccctccc aagcctggga 700

gtaactattt ccccatccc caggcctgtg cccctctctg gtctcgtgct 750

tgtggcagct ctgtcttcag ttctgggata tgtgccctg tggtatgctc 800

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aaaataataa taataataat tcagactcct tatcaggagt ccatgatctg 1350  
gcctggcaca gtaactcatg cctgtaatcc caacattttg ggaggccaac 1400  
gcaggaggat tgcttgaggt ctggaggttt gagaccagcc tgggcaacat 1450  
agaaagaccc catctctaaa taaatgtttt aaaaat 1486

<210> 346

<211> 124

<212> PRT

<213> Homo sapiens

<400> 346

Met	Glu	Leu	Pro	Phe	Val	Thr	His	Leu	Phe	Leu	Pro	Leu	Val	Phe
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Leu	Thr	Gly	Leu	Cys	Ser	Pro	Phe	Asn	Leu	Asp	Glu	His	His	Pro
			20						25					30
Arg	Leu	Phe	Pro	Gly	Pro	Pro	Glu	Ala	Glu	Phe	Gly	Tyr	Ser	Val
			35						40					45
Leu	Gln	His	Val	Gly	Gly	Gly	Gln	Arg	Trp	Met	Leu	Val	Gly	Ala
			50						55					60
Pro	Trp	Asp	Gly	Pro	Ser	Gly	Asp	Arg	Arg	Gly	Asp	Val	Tyr	Arg
			65						70					75
Cys	Pro	Val	Gly	Gly	Ala	His	Asn	Ala	Pro	Cys	Ala	Lys	Gly	His
			80						85					90
Leu	Gly	Asp	Tyr	Gln	Leu	Gly	Asn	Ser	Ser	His	Pro	Ala	Val	Asn
			95						100					105
Met	His	Leu	Gly	Met	Ser	Leu	Leu	Glu	Thr	Asp	Gly	Asp	Gly	Gly
			110						115					120

Phe Met Val Ser

<210> 347  
<211> 509  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 22  
<223> unknown base

<400> 347  
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ggcatggaac tccccttcgt cactcacctg ttcttgcccc tgggtgttct 200  
gacaggtctc tgctccccct ttaacctgga tgaacatcac ccacgcctat 250  
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aggcgaccgg aggggggacg tttatcgctg ccctgtaggg ggggccca 400  
atgccccatg tgccaagggc cacttaggtg actaccaact gggaaattca 450  
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tggtgatgg 509

<210> 348  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 348  
agggacagag gccagaggac ttc 23

<210> 349  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 349  
caggtgcata ttcacagcag gatg 24

<210> 350  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 350  
ggaactcccc ttcgtcactc acctgttctt gcccctggtg ttcct 45

<210> 351  
<211> 2056  
<212> DNA  
<213> Homo sapiens

<400> 351  
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catctggggtt tgggcagaaa ggagggtgct tcggagcccg ccctttctga 100  
gcttctctggg ccggctctag aacaattcag gcttcgctgc gactcagacc 150  
tcagctccaa catatgcatt ctgaagaaag atggctgaga tggacagaat 200  
gctttatttt ggaaagaaac aatgttctag gtcaaactga gtctaccaa 250  
tgcagacttt cacaatgggt ctagaagaaa tctggacaag tcttttcatg 300  
tggtttttct acgcattgat tccatgtttg ctcacagatg aagtggccat 350  
tctgcctgcc ctcagaacc tctctgtact ctcaaccaac atgaagcatc 400  
tcttgatgtg gagcccagtg atcgcgcctg gagaaacagt gtactattct 450  
gtcgaatacc agggggagta cgagagcctg tacacgagcc acatctggat 500  
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atgacatcac ggccactgtg ccatacaacc ttcgtgtcag ggccacattg 600  
ggctcacaga cctcagcctg gagcatcctg aagcatccct ttaatagaaa 650  
ctcaaccatc cttacccgac ctgggatgga gatcaccaa gatggcttcc 700  
acctggttat tgagctggag gacctggggc ccagtttga gttccttggt 750  
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gagtgggggt attccagtgc acctagaaac catggagcca ggggctgcat 850  
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 gagcctgttg tctacaagtc tagaagcaac catcagaggc aggggtggtt 1350  
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 ggctgccact tgctggctga gcaacctgg gaaaagtgc ttcacccctt 1450  
 cggtcctaag ttttctcctc tgtaatgggg gaattaccta cacacctgct 1500  
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 aaaaaa 2056

<210> 352

<211> 311

<212> PRT

<213> Homo sapiens

<400> 352

Met	Gln	Thr	Phe	Thr	Met	Val	Leu	Glu	Glu	Ile	Trp	Thr	Ser	Leu
1					5					10				15

Phe	Met	Trp	Phe	Phe	Tyr	Ala	Leu	Ile	Pro	Cys	Leu	Leu	Thr	Asp
					20				25					30



Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser	35	40	45
Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro	50	55	60
Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu	65	70	75
Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser	80	85	90
Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala	95	100	105
Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln	110	115	120
Thr Ser Ala Trp Ser Ile Leu Lys His Pro Phe Asn Arg Asn Ser	125	130	135
Thr Ile Leu Thr Arg Pro Gly Met Glu Ile Thr Lys Asp Gly Phe	140	145	150
His Leu Val Ile Glu Leu Glu Asp Leu Gly Pro Gln Phe Glu Phe	155	160	165
Leu Val Ala Tyr Trp Arg Arg Glu Pro Gly Ala Glu Glu His Val	170	175	180
Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu Glu Thr Met	185	190	195
Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe Val Lys	200	205	210
Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val Glu	215	220	225
Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe	230	235	240
Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp	245	250	255
Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val	260	265	270
Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile	275	280	285
Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met	290	295	300
Ser Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser	305	310	

<210> 353  
<211> 864  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 654, 711, 748, 827  
<223> unknown base

<400> 353  
tcctgctgat gcacatctgg gtttggcaaa aggaggttgc ttcgagccgc 50  
cctttctagc ttctggccg gctctagaac aattcaggct tcgctgcgac 100  
tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150  
agaatgcttt attttggaaa gaaacaatgt tctaggtcaa actgagtcta 200  
ccaaatgcag actttcacia tggttctaga agaaatctgg acaagtcttt 250  
tcatgtggtt tttctacgca ttgattccat gtttgctcac agatgaagtg 300  
gccattctgc ctgccctca gaacctctct gtactctcaa ccaacatgaa 350  
gcatctcttg atgtggagcc cagtgatcgc gcctggagaa acagtgtact 400  
attctgtcga ataccagggg gactacgaga gcctgtacac gagccacatc 450  
tggatcccca gcagctggtg ctactcact gaaggtcctg agtgtgatgt 500  
cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggcca 550  
cattgggctc acagacctca gcctggagca tcctgaagca tccctttaat 600  
agaaactcaa ccatccttac ccgacctggg atggagatca ccaaagatgg 650  
cttncacctg gttattgagc tggaggacct ggggccccag tttgagttcc 700  
ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750  
gaacccttg cggccgctgg ggtatctctc gagaaaagag aggccaata 800  
tgaccacat actcaatatg gacgaantgc tattgtccac ctgtttgagt 850  
ggcgctgggt tgat 864

<210> 354  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 354  
aggcttcgct gcgactagac ctc 23

<210> 355  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 355  
ccaggtcggg taaggatggt tgag 24

<210> 356  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 356  
tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 357  
<211> 1670  
<212> DNA  
<213> Homo sapiens

<400> 357  
cccacgcgtc cgcccacgcg tccgaggagc aagagagaag agagactgaa 50  
acagggagaa gaggcaggag aggaggaggt ggggagagca cgaagctgga 100  
ggccgacact gagggagggc gggaggaggt gaagaaggag agaggggaga 150  
agaggcagga gctggaaagg agagaggag gaggaggag agatgcggga 200  
tgagacctg gagttaggtg gcttgggaga gcttaatgaa aagagaacgg 250  
agaggaggtg tgggttagga accaagaggt agccctgtgg gcagcagaag 300  
gctgagagga gtaggaagat caggagctag agggagactg gagggttccg 350  
ggaaaagagc agaggaaaga ggaaagacac agagagacgg gagagagaag 400  
aagagtgggt ttgaaggcg gatctcagtc cctggctgct ttggcatttg 450  
gggaactggg actccctgtg gggaggagag gaaagctgga agtcctggag 500  
ggacagggtc ccagaaggag gggacagagg agctgagaga ggggggcagg 550  
gcgttgggca ggggtccctc ggaggcctcc tggggatggg ggctgcagct 600  
cgtctgagcg cccctcgagc gctggtactc tgggctgcac tgggggcagc 650  
agctcacatc ggaccagcac ctgacccga ggactggtgg agctacaagg 700

ataatctcca gggaaacttc gtgccagggc ctcctttctg gggcctggtg 750  
 aatgcagcgt ggagtctgtg tgctgtgggg aagcggcaga gccccgtgga 800  
 tgtggagctg aagagggttc tttatgaccc ctttctgccc ccattaaggc 850  
 tcagcactgg aggagagaag ctccggggaa ctttgtacaa caccggccga 900  
 catgtctcct tcctgctgc accccgacct gtggtcaatg tgtctggagg 950  
 tccccctcct tacagccacc gactcagtga actgcggctg ctgtttggag 1000  
 ctcgcgacgg agccggctcg gaacatcaga tcaaccacca gggcttctct 1050  
 gctgaggtgc agctcattca cttcaaccag gaactctacg ggaatttcag 1100  
 cgctgcctcc cgcgccccca atggcctggc cattctcagc ctctttgtca 1150  
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 accatcactc gcatctccta caagaatgat gcctactttc ttcaagacct 1250  
 gagcctggag ctctgttcc ctgaatcctt cggcttcac acctatcagg 1300  
 gctctctcag caccocgccc tgctccgaga ctgtcacctg gatcctcatt 1350  
 gaccgggccc tcaatatcac ctcccttcag atgcactccc tgagactcct 1400  
 gagccagaat cctccatctc agatcttcca gagcctcagc ggtaacagcc 1450  
 ggcccctgca gcccttgccc cacagggcac tgaggggcaa cagggaacccc 1500  
 cggcaccocg agaggcgctg ccgaggcccc aactaccgcc tgcattgtgga 1550  
 tgggtgtcccc catggtcgct gagactcccc ttcgaggatt gcaccgccc 1600  
 gtctaagcc tccccacaag gcgaggggag ttaccacctaa aacaaagcta 1650  
 ttaaaggagac agaatactta 1670

<210> 358

<211> 328

<212> PRT

<213> Homo sapiens

<400> 358

Met	Gly	Ala	Ala	Ala	Arg	Leu	Ser	Ala	Pro	Arg	Ala	Leu	Val	Leu
1					5				10					15

Trp	Ala	Ala	Leu	Gly	Ala	Ala	Ala	His	Ile	Gly	Pro	Ala	Pro	Asp
				20					25					30

Pro	Glu	Asp	Trp	Trp	Ser	Tyr	Lys	Asp	Asn	Leu	Gln	Gly	Asn	Phe
				35					40					45

Val	Pro	Gly	Pro	Pro	Phe	Trp	Gly	Leu	Val	Asn	Ala	Ala	Trp	Ser
				50					55					60

Leu Cys Ala Val Gly Lys Arg Gln Ser Pro Val Asp Val Glu Leu	65	70	75
Lys Arg Val Leu Tyr Asp Pro Phe Leu Pro Pro Leu Arg Leu Ser	80	85	90
Thr Gly Gly Glu Lys Leu Arg Gly Thr Leu Tyr Asn Thr Gly Arg	95	100	105
His Val Ser Phe Leu Pro Ala Pro Arg Pro Val Val Asn Val Ser	110	115	120
Gly Gly Pro Leu Leu Tyr Ser His Arg Leu Ser Glu Leu Arg Leu	125	130	135
Leu Phe Gly Ala Arg Asp Gly Ala Gly Ser Glu His Gln Ile Asn	140	145	150
His Gln Gly Phe Ser Ala Glu Val Gln Leu Ile His Phe Asn Gln	155	160	165
Glu Leu Tyr Gly Asn Phe Ser Ala Ala Ser Arg Gly Pro Asn Gly	170	175	180
Leu Ala Ile Leu Ser Leu Phe Val Asn Val Ala Ser Thr Ser Asn	185	190	195
Pro Phe Leu Ser Arg Leu Leu Asn Arg Asp Thr Ile Thr Arg Ile	200	205	210
Ser Tyr Lys Asn Asp Ala Tyr Phe Leu Gln Asp Leu Ser Leu Glu	215	220	225
Leu Leu Phe Pro Glu Ser Phe Gly Phe Ile Thr Tyr Gln Gly Ser	230	235	240
Leu Ser Thr Pro Pro Cys Ser Glu Thr Val Thr Trp Ile Leu Ile	245	250	255
Asp Arg Ala Leu Asn Ile Thr Ser Leu Gln Met His Ser Leu Arg	260	265	270
Leu Leu Ser Gln Asn Pro Pro Ser Gln Ile Phe Gln Ser Leu Ser	275	280	285
Gly Asn Ser Arg Pro Leu Gln Pro Leu Ala His Arg Ala Leu Arg	290	295	300
Gly Asn Arg Asp Pro Arg His Pro Glu Arg Arg Cys Arg Gly Pro	305	310	315
Asn Tyr Arg Leu His Val Asp Gly Val Pro His Gly Arg	320	325	

<210> 359

<211> 24

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 359  
tctgctgagg tgcagctcat tcac 24

<210> 360  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 360  
gaggctctgg aagatctgag atgg 24

<210> 361  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 361  
gcctctttgt caacgttgcc agtacctcta acccattcct cagtcgcctc 50

<210> 362  
<211> 3038  
<212> DNA  
<213> Homo sapiens

<400> 362  
ggcgcttggg tctgcgcgta ctggctgtac ggagcaggag caagaggtcg 50  
ccgccagcct ccgccgccga gcctcggttcg tgtccccgcc cctcgctcct 100  
gcagctactg ctcaaaaacg ctggggcgcc caccctggca gactaacgaa 150  
gcagctccct tcccacccca actgcaggtc taattttgga cgctttgcct 200  
gccatttctt ccaggttgag ggagccgcag aggcggaggc tcgcgtattc 250  
ctgcagtcag caccacgctc gccccggac gctcgggtgct caggcccttc 300  
gcgagcgggg ctctccgtct gcggtccttt gtgaaggctc tgggcggctg 350  
cagaggccgg ccgtccggtt tggctcacct ctcccaggaa acttcacact 400  
ggagagccaa aaggagtggg agagcctgtc ttggagattt tcctggggaa 450  
atcctgaggt cattcattat gaagtgtacc gcgcgggagt ggctcagagt 500

aaccacagtg ctgttcatgg ctagagcaat tccagccatg gtggttccca 550  
atgccacttt attggagaaa cttttggaaa aatacatgga tgaggatggt 600  
gagtgggtgga tagccaaaca acgagggaaa agggccatca cagacaatga 650  
catgcagagt attttggacc ttcataataa attacgaagt caggtgtatc 700  
caacagcctc taatatggag tatatgacat gggatgtaga gctggaaaga 750  
tctgcagaat cctgggctga aagttgcttg tgggaacatg gacctgcaag 800  
cttgcttcca tcaattggac agaatttggg agcacactgg ggaagatata 850  
ggcccccgac gtttcatgta caatcgtggt atgatgaagt gaaagacttt 900  
agctacccat atgaacatga atgcaacca tattgtccat tcaggtgttc 950  
tggccctgta tgtacacatt atacacaggt cgtgtgggca actagtaaca 1000  
gaatcggttg tgccattaat ttgtgtcata acatgaacat ctgggggcag 1050  
atatggccca aagctgtcta cctggtgtgc aattactccc caaagggaaa 1100  
ctggtggggc catgcccctt acaaacatgg gcggccctgt tctgcttgcc 1150  
cacctagttt tggagggggc tgtagagaaa atctgtgcta caaagaaggg 1200  
tcagacaggt attatcccc tcgagaagag gaaacaaatg aaatagaacg 1250  
acagcagtca caagtccatg acacccatgt ccggacaaga tcagatgata 1300  
gtagcagaaa tgaagtcata agcgcacagc aaatgtcca aattgtttct 1350  
tgtgaagtaa gattaagaga tcagtgcaa ggaacaacct gcaataggta 1400  
cgaatgtcct gctggctggt tggatagtaa agctaaagtt attggcagtg 1450  
tacattatga aatgcaatcc agcatctgta gagctgcaat tcattatggt 1500  
ataatagaca atgatggtg ctgggtagat atcactagac aaggaagaaa 1550  
gcattatttc atcaagtcca atagaaatgg tattcaaaca attggcaaat 1600  
atcagtctgc taattccttc acagtctcta aagtaacagt tcaggctgtg 1650  
acttgtgaaa caactgtgga acagctctgt ccatttcata agcctgcttc 1700  
acattgcccc agagtatact gtcctcgtaa ctgtatgcaa gcaaatccac 1750  
attatgctcg tgtaattgga actcgagttt attctgatct gtccagtatc 1800  
tgcagagcag cagtacatgc tggagtgggt cgaaatcacg gtggttatgt 1850  
tgatgtaatg cctgtggaca aaagaaagac ctacattgct tcttttcaga 1900  
atggaatctt ctcagaaagt ttacagaatc ctccaggagg aaaggcattc 1950

agagtgtttg ctgttgtgtg aaactgaata cttggaagag gaccataaag 2000  
 actattccaa atgcaatatt tctgaatttt gtataaaact gtaacattac 2050  
 tgtacagagt acatcaacta ttttcagccc aaaaaggtgc caaatgcata 2100  
 taaatcttga taaacaaagt ctataaaata aaacatggga cattagcttt 2150  
 gggaaaagta atgaaaatat aatggtttta gaaatcctgt gttaaattatt 2200  
 gctatatttt cttagcagtt atttctacag ttaattacat agtcatgatt 2250  
 gttctacgtt tcatatatta tatgggtgctt tgtatatgcc actaataaaa 2300  
 tgaatctaaa cattgaatgt gaatggccct cagaaaatca tctagtgcac 2350  
 ttaaaaataa tcgactctaa aactgaaaga aaccttatca cattttcccc 2400  
 agttcaatgc tatgccatta ccaactccaa ataatctcaa ataattttcc 2450  
 acttaataac tgtaaagttt ttttctgtta atttaggcat atagaattatt 2500  
 aaattctgat attgcacttc ttattttata taaaataatc ctttaatatc 2550  
 caaatgaatc tgtaaaatg tttgattcct tgggaatggc cttaaaaata 2600  
 aatgtaataa agtcagagtg gtggtatgaa aacattccta gtgatcatgt 2650  
 agtaaagtga ggggttaagca tggacagcca gagctttcta tgtactgtta 2700  
 aaattgaggt cacatatattt cttttgtatc ctggcaaata ctctgcagg 2750  
 ccaggaagta taatagcaaa aagttgaaca aagatgaact aatgtattac 2800  
 attaccattg ccaactgattt tttttaaatg gttaatgacc ttgtatataa 2850  
 atattgccat atcatggtac ctataatggg gatatatattg tttctatgaa 2900  
 aaatgtattg tgctttgata ctaaaaatct gtaaaatgtt agttttggta 2950  
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 taaacattaa aattaatcat gtttcaaaaa aaaaaaaaa 3038

<210> 363

<211> 500

<212> PRT

<213> Homo sapiens

<400> 363

Met	Lys	Cys	Thr	Ala	Arg	Glu	Trp	Leu	Arg	Val	Thr	Thr	Val	Leu
1				5				10					15	

Phe	Met	Ala	Arg	Ala	Ile	Pro	Ala	Met	Val	Val	Pro	Asn	Ala	Thr
				20				25					30	



Leu	Leu	Glu	Lys	Leu	Leu	Glu	Lys	Tyr	Met	Asp	Glu	Asp	Gly	Glu			
				35					40					45			
Trp	Trp	Ile	Ala	Lys	Gln	Arg	Gly	Lys	Arg	Ala	Ile	Thr	Asp	Asn			
				50					55					60			
Asp	Met	Gln	Ser	Ile	Leu	Asp	Leu	His	Asn	Lys	Leu	Arg	Ser	Gln			
				65					70					75			
Val	Tyr	Pro	Thr	Ala	Ser	Asn	Met	Glu	Tyr	Met	Thr	Trp	Asp	Val			
				80					85					90			
Glu	Leu	Glu	Arg	Ser	Ala	Glu	Ser	Trp	Ala	Glu	Ser	Cys	Leu	Trp			
				95					100					105			
Glu	His	Gly	Pro	Ala	Ser	Leu	Leu	Pro	Ser	Ile	Gly	Gln	Asn	Leu			
				110					115					120			
Gly	Ala	His	Trp	Gly	Arg	Tyr	Arg	Pro	Pro	Thr	Phe	His	Val	Gln			
				125					130					135			
Ser	Trp	Tyr	Asp	Glu	Val	Lys	Asp	Phe	Ser	Tyr	Pro	Tyr	Glu	His			
				140					145					150			
Glu	Cys	Asn	Pro	Tyr	Cys	Pro	Phe	Arg	Cys	Ser	Gly	Pro	Val	Cys			
				155					160					165			
Thr	His	Tyr	Thr	Gln	Val	Val	Trp	Ala	Thr	Ser	Asn	Arg	Ile	Gly			
				170					175					180			
Cys	Ala	Ile	Asn	Leu	Cys	His	Asn	Met	Asn	Ile	Trp	Gly	Gln	Ile			
				185					190					195			
Trp	Pro	Lys	Ala	Val	Tyr	Leu	Val	Cys	Asn	Tyr	Ser	Pro	Lys	Gly			
				200					205					210			
Asn	Trp	Trp	Gly	His	Ala	Pro	Tyr	Lys	His	Gly	Arg	Pro	Cys	Ser			
				215					220					225			
Ala	Cys	Pro	Pro	Ser	Phe	Gly	Gly	Gly	Cys	Arg	Glu	Asn	Leu	Cys			
				230					235					240			
Tyr	Lys	Glu	Gly	Ser	Asp	Arg	Tyr	Tyr	Pro	Pro	Arg	Glu	Glu	Glu			
				245					250					255			
Thr	Asn	Glu	Ile	Glu	Arg	Gln	Gln	Ser	Gln	Val	His	Asp	Thr	His			
				260					265					270			
Val	Arg	Thr	Arg	Ser	Asp	Asp	Ser	Ser	Arg	Asn	Glu	Val	Ile	Ser			
				275					280					285			
Ala	Gln	Gln	Met	Ser	Gln	Ile	Val	Ser	Cys	Glu	Val	Arg	Leu	Arg			
				290					295					300			
Asp	Gln	Cys	Lys	Gly	Thr	Thr	Cys	Asn	Arg	Tyr	Glu	Cys	Pro	Ala			
				305					310					315			

Gly Cys Leu Asp Ser Lys Ala Lys Val	Ile Gly Ser Val His Tyr
320	325 330
Glu Met Gln Ser Ser Ile Cys Arg Ala	Ala Ile His Tyr Gly Ile
335	340 345
Ile Asp Asn Asp Gly Gly Trp Val Asp	Ile Thr Arg Gln Gly Arg
350	355 360
Lys His Tyr Phe Ile Lys Ser Asn Arg	Asn Gly Ile Gln Thr Ile
365	370 375
Gly Lys Tyr Gln Ser Ala Asn Ser Phe	Thr Val Ser Lys Val Thr
380	385 390
Val Gln Ala Val Thr Cys Glu Thr Thr	Val Glu Gln Leu Cys Pro
395	400 405
Phe His Lys Pro Ala Ser His Cys Pro	Arg Val Tyr Cys Pro Arg
410	415 420
Asn Cys Met Gln Ala Asn Pro His Tyr	Ala Arg Val Ile Gly Thr
425	430 435
Arg Val Tyr Ser Asp Leu Ser Ser Ile	Cys Arg Ala Ala Val His
440	445 450
Ala Gly Val Val Arg Asn His Gly Gly	Tyr Val Asp Val Met Pro
455	460 465
Val Asp Lys Arg Lys Thr Tyr Ile Ala	Ser Phe Gln Asn Gly Ile
470	475 480
Phe Ser Glu Ser Leu Gln Asn Pro Pro	Gly Gly Lys Ala Phe Arg
485	490 495
Val Phe Ala Val Val	
500	

<210> 364

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 364

ggacagaatt tgggagcaca ctgg 24

<210> 365

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 365  
ccaagagtat actgtcctcg 20

<210> 366  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 366  
agcacagatt ttctctacag ccccc 25

<210> 367  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 367  
aaccactcca gcatgtactg ctgc 24

<210> 368  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 368  
ccattcaggt gttctggccc tgtatgtaca cattatacac aggtcgtgtg 50

<210> 369  
<211> 1685  
<212> DNA  
<213> Homo sapiens

<400> 369  
gcggagacaa gcgcagagcg cagcgcacgg ccacagacag ccctgggcat 50  
ccaccgacgg cgcagccgga gccagcagag ccggaaggcg cgccccgggc 100  
agagaaagcc gagcagagct ggggtggcgtc tccgggccgc cgctccgacg 150  
ggccagcgcc ctcccatgt ccctgctccc acgccgcgcc cctccggtca 200  
gcatgaggct cctggcgggc gcgctgctcc tgctgctgct ggcgctgtac 250  
accgcgcgtg tggacgggtc caaatgcaag tgctcccga agggacccaa 300  
gatccgctac agcgacgtga agaagctgga aatgaagcca aagtaccgc 350

actgcgagga gaagatgggtt atcatcacca ccaagagcgt gtccaggtac 400  
 cgagggtcagg agcactgcct gcacccaag ctgcagagca ccaagcgctt 450  
 catcaagtgg tacaacgcct ggaacgagaa gcgcagggtc tacgaagaat 500  
 aggggtgaaaa acctcagaag ggaaaaactcc aaaccagttg ggagacttgt 550  
 gcaaaggact ttgcagatta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 600  
 aaaaaaaaaa aaagcctttc tttctcacag gcataagaca caaattatat 650  
 attgttatga agcacttttt accaacgggtc agttttttaca ttttatagct 700  
 gcgtgcgaaa ggcttcaga tgggagaccc atctctcttg tgctccagac 750  
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 ttttaaaaaa tgcttttttg tatttgtcca tacgtcacta tacatctgag 850  
 ctttataagc gcccgggagg aacaatgagc ttggtggaca catttcattg 900  
 cagtgttgct ccattcctag cttgggaagc ttccgcttag aggtcctggc 950  
 gcctcggcac agctgccag ggctctcctg ggcttatggc cggtcacagc 1000  
 ctcaagtga ctccacagtg gccctgtag ccgggcaagc aggagcaggt 1050  
 ctctctgcat ctgttctctg aggaactcaa gtttggttgc cagaaaaatg 1100  
 tgcttcattc cccctgggtt aattttttaca caccctagga aacatttcca 1150  
 agatcctgtg atggcgagac aaatgatcct taaagaaggt gtgggggtctt 1200  
 tccaacctg aggatttctg aaagggtcac aggttcaata tttaatgctt 1250  
 cagaagcatg tgagggtccc aacactgtca gcaaaaacct taggagaaaa 1300  
 cttaaaaaata tatgaataca tgcgcaatac acagctacag acacacattc 1350  
 tggtgacaag ggaaaacctt caaagcatgt ttctttccct caccacaaca 1400  
 gaacatgcag tactaaagca atatatttgt gattcccat gtaattottc 1450  
 aatgttaaac agtgcagtcc tctttcgaaa gctaagatga ccatgcgccc 1500  
 tttcctctgt acatataccc ttaagaacgc cccctccaca cactgcccc 1550  
 cagtatatgc cgcattgtac tgctgtgtta tatgctatgt acatgtcaga 1600  
 aaccattagc attgcatgca ggtttcatat tctttctaag atggaaagta 1650  
 ataaaatata ttgaaatgt aaaaaaaaaa aaaaa 1685

<210> 370

<211> 111

<212> PRT

<213> Homo sapiens

<400> 370

Met	Ser	Leu	Leu	Pro	Arg	Arg	Ala	Pro	Pro	Val	Ser	Met	Arg	Leu	
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Leu	Ala	Ala	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Leu	Tyr	Thr	Ala	
				20					25					30	
Arg	Val	Asp	Gly	Ser	Lys	Cys	Lys	Cys	Ser	Arg	Lys	Gly	Pro	Lys	
				35					40					45	
Ile	Arg	Tyr	Ser	Asp	Val	Lys	Lys	Leu	Glu	Met	Lys	Pro	Lys	Tyr	
				50					55					60	
Pro	His	Cys	Glu	Glu	Lys	Met	Val	Ile	Ile	Thr	Thr	Lys	Ser	Val	
				65					70					75	
Ser	Arg	Tyr	Arg	Gly	Gln	Glu	His	Cys	Leu	His	Pro	Lys	Leu	Gln	
				80					85					90	
Ser	Thr	Lys	Arg	Phe	Ile	Lys	Trp	Tyr	Asn	Ala	Trp	Asn	Glu	Lys	
				95					100					105	
Arg	Arg	Val	Tyr	Glu	Glu										
				110											

<210> 371

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 371

cagcgccctc cccatgtccc tg 22

<210> 372

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 372

tcccaactgg tttggagttt tccc 24

<210> 373

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 373  
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<210> 374  
<211> 3113  
<212> DNA  
<213> Homo sapiens

<400> 374  
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accctcattg acagccaagc acagtatcca gttgtcaaca caaattatgg 150  
caaaatccgg ggcctaagaa caccgttacc caatgagatc ttgggtccag 200  
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cggtttcagc cccagaacc cccgtcctcc tggactggca tccgaaatac 300  
tactcagttt gctgctgtgt gccccagca cctggatgag agatccttac 350  
tgcatgacat gctgcccac tggtttaccg ccaatttgga tactttgatg 400  
acctatgttc aagatcaaaa tgaagactgc ctttacttaa acatctacgt 450  
gcccacggaa gatggagcca acacaaagaa aaacgcagat gatataacga 500  
gtaatgaccg tgggtgaagac gaagatatc atgatcagaa cagtaagaag 550  
cccgatcatgg tctatatcca tgggggatct tacatggagg gcaccggcaa 600  
catgattgac ggcagcattt tggcaagcta cggaaacgtc atcgtgatca 650  
ccattaacta ccgtctggga atactagggt ttttaagtac cggtgaccag 700  
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tctttggctc gggggctggg gcctcctgtg tcagcctgtt gaccctgtcc 850  
cactactcag aaggtctctt ccagaaggcc atcattcaga gcggcaccgc 900  
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tgcttgcgga acaagaacta caaggagctc atccagcaga ccatcaccac 1050  
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cgtggataac gaggacggtg tgacgccccaa cgactttgac ttctccgtgt 1250  
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acaagaggcg ccatgagact cacaggcgcc ccagtccca gagaaacacc 2200  
acaaatgata tcgtcacat ccagaacgaa gagatcatgt ctctgcagat 2250  
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 agagaaggaa acgtagaaat ttattattaa aagaatggac tgtgcagcga 3050  
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 taagagactt tgt 3113

<210> 375

<211> 816

<212> PRT

<213> Homo sapiens

<400> 375

Met	Leu	Asn	Ser	Asn	Val	Leu	Leu	Trp	Leu	Thr	Ala	Leu	Ala	Ile	1	5	10	15
Lys	Phe	Thr	Leu	Ile	Asp	Ser	Gln	Ala	Gln	Tyr	Pro	Val	Val	Asn	20	25	30	
Thr	Asn	Tyr	Gly	Lys	Ile	Arg	Gly	Leu	Arg	Thr	Pro	Leu	Pro	Asn	35	40	45	
Glu	Ile	Leu	Gly	Pro	Val	Glu	Gln	Tyr	Leu	Gly	Val	Pro	Tyr	Ala	50	55	60	
Ser	Pro	Pro	Thr	Gly	Glu	Arg	Arg	Phe	Gln	Pro	Pro	Glu	Pro	Pro	65	70	75	
Ser	Ser	Trp	Thr	Gly	Ile	Arg	Asn	Thr	Thr	Gln	Phe	Ala	Ala	Val	80	85	90	
Cys	Pro	Gln	His	Leu	Asp	Glu	Arg	Ser	Leu	Leu	His	Asp	Met	Leu	95	100	105	
Pro	Ile	Trp	Phe	Thr	Ala	Asn	Leu	Asp	Thr	Leu	Met	Thr	Tyr	Val	110	115	120	
Gln	Asp	Gln	Asn	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Ile	Tyr	Val	Pro	125	130	135	
Thr	Glu	Asp	Gly	Ala	Asn	Thr	Lys	Lys	Asn	Ala	Asp	Asp	Ile	Thr	140	145	150	



Ser Asn Asp Arg Gly Glu Asp Glu Asp Ile His Asp Gln Asn Ser	155	160	165
Lys Lys Pro Val Met Val Tyr Ile His Gly Gly Ser Tyr Met Glu	170	175	180
Gly Thr Gly Asn Met Ile Asp Gly Ser Ile Leu Ala Ser Tyr Gly	185	190	195
Asn Val Ile Val Ile Thr Ile Asn Tyr Arg Leu Gly Ile Leu Gly	200	205	210
Phe Leu Ser Thr Gly Asp Gln Ala Ala Lys Gly Asn Tyr Gly Leu	215	220	225
Leu Asp Gln Ile Gln Ala Leu Arg Trp Ile Glu Glu Asn Val Gly	230	235	240
Ala Phe Gly Gly Asp Pro Lys Arg Val Thr Ile Phe Gly Ser Gly	245	250	255
Ala Gly Ala Ser Cys Val Ser Leu Leu Thr Leu Ser His Tyr Ser	260	265	270
Glu Gly Leu Phe Gln Lys Ala Ile Ile Gln Ser Gly Thr Ala Leu	275	280	285
Ser Ser Trp Ala Val Asn Tyr Gln Pro Ala Lys Tyr Thr Arg Ile	290	295	300
Leu Ala Asp Lys Val Gly Cys Asn Met Leu Asp Thr Thr Asp Met	305	310	315
Val Glu Cys Leu Arg Asn Lys Asn Tyr Lys Glu Leu Ile Gln Gln	320	325	330
Thr Ile Thr Pro Ala Thr Tyr His Ile Ala Phe Gly Pro Val Ile	335	340	345
Asp Gly Asp Val Ile Pro Asp Asp Pro Gln Ile Leu Met Glu Gln	350	355	360
Gly Glu Phe Leu Asn Tyr Asp Ile Met Leu Gly Val Asn Gln Gly	365	370	375
Glu Gly Leu Lys Phe Val Asp Gly Ile Val Asp Asn Glu Asp Gly	380	385	390
Val Thr Pro Asn Asp Phe Asp Phe Ser Val Ser Asn Phe Val Asp	395	400	405
Asn Leu Tyr Gly Tyr Pro Glu Gly Lys Asp Thr Leu Arg Glu Thr	410	415	420
Ile Lys Phe Met Tyr Thr Asp Trp Ala Asp Lys Glu Asn Pro Glu	425	430	435

Thr Arg Arg Lys	Thr Leu Val Ala Leu	Phe Thr Asp His Gln Trp	
440		445	450
Val Ala Pro Ala	Val Ala Ala Asp Leu	His Ala Gln Tyr Gly Ser	
455		460	465
Pro Thr Tyr Phe	Tyr Ala Phe Tyr His	His Cys Gln Ser Glu Met	
470		475	480
Lys Pro Ser Trp	Ala Asp Ser Ala His	Gly Asp Glu Val Pro Tyr	
485		490	495
Val Phe Gly Ile	Pro Met Ile Gly Pro	Thr Glu Leu Phe Ser Cys	
500		505	510
Asn Phe Ser Lys	Asn Asp Val Met Leu	Ser Ala Val Val Met Thr	
515		520	525
Tyr Trp Thr Asn	Phe Ala Lys Thr Gly	Asp Pro Asn Gln Pro Val	
530		535	540
Pro Gln Asp Thr	Lys Phe Ile His Thr	Lys Pro Asn Arg Phe Glu	
545		550	555
Glu Val Ala Trp	Ser Lys Tyr Asn Pro	Lys Asp Gln Leu Tyr Leu	
560		565	570
His Ile Gly Leu	Lys Pro Arg Val Arg	Asp His Tyr Arg Ala Thr	
575		580	585
Lys Val Ala Phe	Trp Leu Glu Leu Val	Pro His Leu His Asn Leu	
590		595	600
Asn Glu Ile Phe	Gln Tyr Val Ser Thr	Thr Thr Lys Val Pro Pro	
605		610	615
Pro Asp Met Thr	Ser Phe Pro Tyr Gly	Thr Arg Arg Ser Pro Ala	
620		625	630
Lys Ile Trp Pro	Thr Thr Lys Arg Pro	Ala Ile Thr Pro Ala Asn	
635		640	645
Asn Pro Lys His	Ser Lys Asp Pro His	Lys Thr Gly Pro Glu Asp	
650		655	660
Thr Thr Val Leu	Ile Glu Thr Lys Arg	Asp Tyr Ser Thr Glu Leu	
665		670	675
Ser Val Thr Ile	Ala Val Gly Ala Ser	Leu Leu Phe Leu Asn Ile	
680		685	690
Leu Ala Phe Ala	Ala Leu Tyr Tyr Lys	Lys Asp Lys Arg Arg His	
695		700	705
Glu Thr His Arg	Arg Pro Ser Pro Gln	Arg Asn Thr Thr Asn Asp	
710		715	720

Ile Ala His Ile Gln Asn Glu Glu Ile Met Ser Leu Gln Met Lys  
725 730 735

Gln Leu Glu His Asp His Glu Cys Glu Ser Leu Gln Ala His Asp  
740 745 750

Thr Leu Arg Leu Thr Cys Pro Pro Asp Tyr Thr Leu Thr Leu Arg  
755 760 765

Arg Ser Pro Asp Asp Ile Pro Leu Met Thr Pro Asn Thr Ile Thr  
770 775 780

Met Ile Pro Asn Thr Leu Thr Gly Met Gln Pro Leu His Thr Phe  
785 790 795

Asn Thr Phe Ser Gly Gly Gln Asn Ser Thr Asn Leu Pro His Gly  
800 805 810

His Ser Thr Thr Arg Val  
815

<210> 376

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 376

ggcaagctac ggaaacgtca tcgtg 25

<210> 377

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 377

aacccccgag ccaaaagatg gtcac 25

<210> 378

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 378

gtaccggtga ccaggcagca aaaggcaact atgggctcct ggatcag 47

<210> 379

<211> 2461

<212> DNA

<213> Homo sapiens

<400> 379

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ttgttggggg ctgggcaggg gccacagcaa gtcggggcgg gtcaaacgtt 150  
cgagtacttg aaacgggagc actcgtctgc gaagccctac caggggtgtg 200  
gcacaggcag ttcctcactg tggaatctga tgggcaatgc catggtgatg 250  
accagttata tccgccttac cccagatatg caaagtaaac aggggtgcctt 300  
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ggacaaatth gtggggctgg gaggatthgt agacacctac cccaatgagg 500  
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<210> 380

<211> 348

<212> PRT

<213> Homo sapiens

<400> 380

Met	Ala	Ala	Thr	Leu	Gly	Pro	Leu	Gly	Ser	Trp	Gln	Gln	Trp	Arg
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Arg	Cys	Leu	Ser	Ala	Arg	Asp	Gly	Ser	Arg	Met	Leu	Leu	Leu	Leu
				20				25					30	

Leu	Leu	Leu	Gly	Ser	Gly	Gln	Gly	Pro	Gln	Gln	Val	Gly	Ala	Gly		35	40	45
Gln	Thr	Phe	Glu	Tyr	Leu	Lys	Arg	Glu	His	Ser	Leu	Ser	Lys	Pro		50	55	60
Tyr	Gln	Gly	Val	Gly	Thr	Gly	Ser	Ser	Ser	Leu	Trp	Asn	Leu	Met		65	70	75
Gly	Asn	Ala	Met	Val	Met	Thr	Gln	Tyr	Ile	Arg	Leu	Thr	Pro	Asp		80	85	90
Met	Gln	Ser	Lys	Gln	Gly	Ala	Leu	Trp	Asn	Arg	Val	Pro	Cys	Phe		95	100	105
Leu	Arg	Asp	Trp	Glu	Leu	Gln	Val	His	Phe	Lys	Ile	His	Gly	Gln		110	115	120
Gly	Lys	Lys	Asn	Leu	His	Gly	Asp	Gly	Leu	Ala	Ile	Trp	Tyr	Thr		125	130	135
Lys	Asp	Arg	Met	Gln	Pro	Gly	Pro	Val	Phe	Gly	Asn	Met	Asp	Lys		140	145	150
Phe	Val	Gly	Leu	Gly	Val	Phe	Val	Asp	Thr	Tyr	Pro	Asn	Glu	Glu		155	160	165
Lys	Gln	Gln	Glu	Arg	Val	Phe	Pro	Tyr	Ile	Ser	Ala	Met	Val	Asn		170	175	180
Asn	Gly	Ser	Leu	Ser	Tyr	Asp	His	Glu	Arg	Asp	Gly	Arg	Pro	Thr		185	190	195
Glu	Leu	Gly	Gly	Cys	Thr	Ala	Ile	Val	Arg	Asn	Leu	His	Tyr	Asp		200	205	210
Thr	Phe	Leu	Val	Ile	Arg	Tyr	Val	Lys	Arg	His	Leu	Thr	Ile	Met		215	220	225
Met	Asp	Ile	Asp	Gly	Lys	His	Glu	Trp	Arg	Asp	Cys	Ile	Glu	Val		230	235	240
Pro	Gly	Val	Arg	Leu	Pro	Arg	Gly	Tyr	Tyr	Phe	Gly	Thr	Ser	Ser		245	250	255
Ile	Thr	Gly	Asp	Leu	Ser	Asp	Asn	His	Asp	Val	Ile	Ser	Leu	Lys		260	265	270
Leu	Phe	Glu	Leu	Thr	Val	Glu	Arg	Thr	Pro	Glu	Glu	Glu	Lys	Leu		275	280	285
His	Arg	Asp	Val	Phe	Leu	Pro	Ser	Val	Asp	Asn	Met	Lys	Leu	Pro		290	295	300
Glu	Met	Thr	Ala	Pro	Leu	Pro	Pro	Leu	Ser	Gly	Leu	Ala	Leu	Phe		305	310	315

Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val  
320 325 330

Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys  
335 340 345

Arg Phe Tyr

<210> 381  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 381  
ccttgggtcg tggcagcagt gg 22

<210> 382  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 382  
cactctccag gctgcatgct cagg 24

<210> 383  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 383  
gtcaaacggt cgagtacttg aaacgggagc actcgctgtc gaagc 45

<210> 384  
<211> 3150  
<212> DNA  
<213> Homo sapiens

<400> 384  
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gtgagtgcaa tctacggatc agtctctgat ggtgggtcgt taacctcagt 100  
ggggactcca agatttccat gaagaaaatc agttgtcttc attcaagaat 150  
tggggtctgg ctgcagaattc ctgcagctgg tgaaaatctg ttttctagaa 200

gaggtttaat taatgcctgc agtctgacat gttcccgatt tgaggtgaaa 250  
ccatgaagag aaaatagaat acttaataat gcttttccgc aaccgcttct 300  
tgctgctgct ggccctggct gcgctgctgg cctttgtgag cctcagcctg 350  
cagttcttcc acctgatccc ggtgtcgact cctaagaatg gaatgagtag 400  
caagagtcga aagagaatca tgccccgacc tgtgacggag cccctgtga 450  
cagaccccggt ttatgaagct cttttgtact gcaacatccc cagtgtggcc 500  
gagcgcagca tggaaggctca tgccccgcat cattttaagc tgggtctcagt 550  
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<210> 385

<211> 480

<212> PRT

<213> Homo sapiens

<400> 385

Met	Leu	Phe	Arg	Asn	Arg	Phe	Leu	Leu	Leu	Leu	Ala	Leu	Ala	Ala
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Leu	Leu	Ala	Phe	Val	Ser	Leu	Ser	Leu	Gln	Phe	Phe	His	Leu	Ile
				20					25					30

Pro	Val	Ser	Thr	Pro	Lys	Asn	Gly	Met	Ser	Ser	Lys	Ser	Arg	Lys
				35					40					45

Arg	Ile	Met	Pro	Asp	Pro	Val	Thr	Glu	Pro	Pro	Val	Thr	Asp	Pro
				50					55					60

Val	Tyr	Glu	Ala	Leu	Leu	Tyr	Cys	Asn	Ile	Pro	Ser	Val	Ala	Glu
				65					70					75

Arg	Ser	Met	Glu	Gly	His	Ala	Pro	His	His	Phe	Lys	Leu	Val	Ser
				80					85					90

Val	His	Val	Phe	Ile	Arg	His	Gly	Asp	Arg	Tyr	Pro	Leu	Tyr	Val
				95					100					105

Ile	Pro	Lys	Thr	Lys	Arg	Pro	Glu	Ile	Asp	Cys	Thr	Leu	Val	Ala
				110					115					120

Asn	Arg	Lys	Pro	Tyr	His	Pro	Lys	Leu	Glu	Ala	Phe	Ile	Ser	His
				125					130					135

Met	Ser	Lys	Gly	Ser	Gly	Ala	Ser	Phe	Glu	Ser	Pro	Leu	Asn	Ser
				140					145					150

Leu	Pro	Leu	Tyr	Pro	Asn	His	Pro	Leu	Cys	Glu	Met	Gly	Glu	Leu
				155					160					165

Thr	Gln	Thr	Gly	Val	Val	Gln	His	Leu	Gln	Asn	Gly	Gln	Leu	Leu
				170					175					180

Arg	Asp	Ile	Tyr	Leu	Lys	Lys	His	Lys	Leu	Leu	Pro	Asn	Asp	Trp
				185					190					195

Ser	Ala	Asp	Gln	Leu	Tyr	Leu	Glu	Thr	Thr	Gly	Lys	Ser	Arg	Thr
				200					205					210

Leu	Gln	Ser	Gly	Leu	Ala	Leu	Leu	Tyr	Gly	Phe	Leu	Pro	Asp	Phe
				215					220					225

Asp	Trp	Lys	Lys	Ile	Tyr	Phe	Arg	His	Gln	Pro	Ser	Ala	Leu	Phe
				230					235					240

Cys Ser Gly Ser Cys Tyr Cys Pro Val Arg Asn Gln Tyr Leu Glu	245	250	255
Lys Glu Gln Arg Arg Gln Tyr Leu Leu Arg Leu Lys Asn Ser Gln	260	265	270
Leu Glu Lys Thr Tyr Gly Glu Met Ala Lys Ile Val Asp Val Pro	275	280	285
Thr Lys Gln Leu Arg Ala Ala Asn Pro Ile Asp Ser Met Leu Cys	290	295	300
His Phe Cys His Asn Val Ser Phe Pro Cys Thr Arg Asn Gly Cys	305	310	315
Val Asp Met Glu His Phe Lys Val Ile Lys Thr His Gln Ile Glu	320	325	330
Asp Glu Arg Glu Arg Arg Glu Lys Lys Leu Tyr Phe Gly Tyr Ser	335	340	345
Leu Leu Gly Ala His Pro Ile Leu Asn Gln Thr Ile Gly Arg Met	350	355	360
Gln Arg Ala Thr Glu Gly Arg Lys Glu Glu Leu Phe Ala Leu Tyr	365	370	375
Ser Ala His Asp Val Thr Leu Ser Pro Val Leu Ser Ala Leu Gly	380	385	390
Leu Ser Glu Ala Arg Phe Pro Arg Phe Ala Ala Arg Leu Ile Phe	395	400	405
Glu Leu Trp Gln Asp Arg Glu Lys Pro Ser Glu His Ser Val Arg	410	415	420
Ile Leu Tyr Asn Gly Val Asp Val Thr Phe His Thr Ser Phe Cys	425	430	435
Gln Asp His His Lys Arg Ser Pro Lys Pro Met Cys Pro Leu Glu	440	445	450
Asn Leu Val Arg Phe Val Lys Arg Asp Met Phe Val Ala Leu Gly	455	460	465
Gly Ser Gly Thr Asn Tyr Tyr Asp Ala Cys His Arg Glu Gly Phe	470	475	480

<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 386

ccaagcagct tagagctcca gacc 24

<210> 387

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 387

ttccctatgc tctgtattgg catgg 25

<210> 388

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 388

gccacttctg ccacaatgtc agctttccct gtaccagaaa tggctgtgtt 50

<210> 389

<211> 3313

<212> DNA

<213> Homo sapiens

<400> 389

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cccttttgaa gaacagtact gtggagctat ttaagagata aaaacgaaat 100

atcctttctg ggagttcaag attgtgcagt aattggttag gactctgagc 150

gccgctgttc accaatcggg gagagaaaag cggagatcct gctcgccttg 200

cacgcgcctg aagcacaaag cagatagcta ggaatgaacc atccctggga 250

gtatgtggaa acaacggagg agctctgact tcccaactgt ccattctat 300

gggcgaagga actgctcctg acttcagtgg ttaagggcag aattgaaaat 350

aattctggag gaagataaga atgattcctg cgcgactgca ccgggactac 400

aaagggcttg tctgctggg aatcctcctg gggactctgt gggagaccgg 450

atgcacccag atacgctatt cagttccgga agagctggag aaaggctcta 500

gggtgggcga catctccagg gacctggggc tggagccccg ggagctcgcg 550

gagcgcggag tccgcatcat cccagaggt aggacgcagc ttttcgccct 600

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<210> 390

<211> 916

<212> PRT

<213> Homo sapiens

<400> 390

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Leu	Gly	Ile	Leu	Leu	Gly	Thr	Leu	Trp	Glu	Thr	Gly	Cys	Thr	Gln			
					20				25					30			
Ile	Arg	Tyr	Ser	Val	Pro	Glu	Glu	Leu	Glu	Lys	Gly	Ser	Arg	Val			
					35				40					45			
Gly	Asp	Ile	Ser	Arg	Asp	Leu	Gly	Leu	Glu	Pro	Arg	Glu	Leu	Ala			
					50				55					60			
Glu	Arg	Gly	Val	Arg	Ile	Ile	Pro	Arg	Gly	Arg	Thr	Gln	Leu	Phe			
					65				70					75			
Ala	Leu	Asn	Pro	Arg	Ser	Gly	Ser	Leu	Val	Thr	Ala	Gly	Arg	Ile			
					80				85					90			
Asp	Arg	Glu	Glu	Leu	Cys	Met	Gly	Ala	Ile	Lys	Cys	Gln	Leu	Asn			
					95				100					105			
Leu	Asp	Ile	Leu	Met	Glu	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Val	Glu			
					110				115					120			
Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Tyr	Phe	Arg	Glu			
					125				130					135			
Ser	Glu	Leu	Glu	Ile	Lys	Ile	Ser	Glu	Asn	Ala	Ala	Thr	Glu	Met			
					140				145					150			
Arg	Phe	Pro	Leu	Pro	His	Ala	Trp	Asp	Pro	Asp	Ile	Gly	Lys	Asn			
					155				160					165			
Ser	Leu	Gln	Ser	Tyr	Glu	Leu	Ser	Pro	Asn	Thr	His	Phe	Ser	Leu			
					170				175					180			
Ile	Val	Gln	Asn	Gly	Ala	Asp	Gly	Ser	Lys	Tyr	Pro	Glu	Leu	Val			
					185				190					195			
Leu	Lys	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Lys	Ala	Ala	His	His	Leu			
					200				205					210			
Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Asp	Pro	Val	Arg	Thr	Gly	Thr			
					215				220					225			
Ala	Arg	Ile	Arg	Val	Met	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro			
					230				235					240			
Ala	Phe	Ala	Gln	Pro	Glu	Tyr	Arg	Ala	Ser	Val	Pro	Glu	Asn	Leu			
					245				250					255			
Ala	Leu	Gly	Thr	Gln	Leu	Leu	Val	Val	Asn	Ala	Thr	Asp	Pro	Asp			
					260				265					270			
Glu	Gly	Val	Asn	Ala	Glu	Val	Arg	Tyr	Ser	Phe	Arg	Tyr	Val	Asp			
					275				280					285			

Asp Lys Ala Ala Gln Val Phe Lys Leu	Asp Cys Asn Ser Gly Thr	
290	295	300
Ile Ser Thr Ile Gly Glu Leu Asp His	Glu Glu Ser Gly Phe Tyr	
305	310	315
Gln Met Glu Val Gln Ala Met Asp Asn	Ala Gly Tyr Ser Ala Arg	
320	325	330
Ala Lys Val Leu Ile Thr Val Leu Asp	Val Asn Asp Asn Ala Pro	
335	340	345
Glu Val Val Leu Thr Ser Leu Ala Ser	Ser Val Pro Glu Asn Ser	
350	355	360
Pro Arg Gly Thr Leu Ile Ala Leu Leu	Asn Val Asn Asp Gln Asp	
365	370	375
Ser Glu Glu Asn Gly Gln Val Ile Cys	Phe Ile Gln Gly Asn Leu	
380	385	390
Pro Phe Lys Leu Glu Lys Ser Tyr Gly	Asn Tyr Tyr Ser Leu Val	
395	400	405
Thr Asp Ile Val Leu Asp Arg Glu Gln	Val Pro Ser Tyr Asn Ile	
410	415	420
Thr Val Thr Ala Thr Asp Arg Gly Thr	Pro Pro Leu Ser Thr Glu	
425	430	435
Thr His Ile Ser Leu Asn Val Ala Asp	Thr Asn Asp Asn Pro Pro	
440	445	450
Val Phe Pro Gln Ala Ser Tyr Ser Ala	Tyr Ile Pro Glu Asn Asn	
455	460	465
Pro Arg Gly Val Ser Leu Val Ser Val	Thr Ala His Asp Pro Asp	
470	475	480
Cys Glu Glu Asn Ala Gln Ile Thr Tyr	Ser Leu Ala Glu Asn Thr	
485	490	495
Ile Gln Gly Ala Ser Leu Ser Ser Tyr	Val Ser Ile Asn Ser Asp	
500	505	510
Thr Gly Val Leu Tyr Ala Leu Ser Ser	Phe Asp Tyr Glu Gln Phe	
515	520	525
Arg Asp Leu Gln Val Lys Val Met Ala	Arg Asp Asn Gly His Pro	
530	535	540
Pro Leu Ser Ser Asn Val Ser Leu Ser	Leu Phe Val Leu Asp Gln	
545	550	555
Asn Asp Asn Ala Pro Glu Ile Leu Tyr	Pro Ala Leu Pro Thr Asp	
560	565	570



Gly Ser Thr Gly Val Glu Leu Ala Pro Arg Ser Ala Glu Pro Gly	575	580	585
Tyr Leu Val Thr Lys Val Val Ala Val Asp Arg Asp Ser Gly Gln	590	595	600
Asn Ala Trp Leu Ser Tyr Arg Leu Leu Lys Ala Ser Glu Pro Gly	605	610	615
Leu Phe Ser Val Gly Leu His Thr Gly Glu Val Arg Thr Ala Arg	620	625	630
Ala Leu Leu Asp Arg Asp Ala Leu Lys Gln Ser Leu Val Val Ala	635	640	645
Val Gln Asp His Gly Gln Pro Pro Leu Ser Ala Thr Val Thr Leu	650	655	660
Thr Val Ala Val Ala Asp Ser Ile Pro Gln Val Leu Ala Asp Leu	665	670	675
Gly Ser Leu Glu Ser Pro Ala Asn Ser Glu Thr Ser Asp Leu Thr	680	685	690
Leu Tyr Leu Val Val Ala Val Ala Ala Val Ser Cys Val Phe Leu	695	700	705
Ala Phe Val Ile Leu Leu Leu Ala Leu Arg Leu Arg Arg Trp His	710	715	720
Lys Ser Arg Leu Leu Gln Ala Ser Gly Gly Gly Leu Thr Gly Ala	725	730	735
Pro Ala Ser His Phe Val Gly Val Asp Gly Val Gln Ala Phe Leu	740	745	750
Gln Thr Tyr Ser His Glu Val Ser Leu Thr Thr Asp Ser Arg Lys	755	760	765
Ser His Leu Ile Phe Pro Gln Pro Asn Tyr Ala Asp Met Leu Val	770	775	780
Ser Gln Glu Ser Phe Glu Lys Ser Glu Pro Leu Leu Leu Ser Gly	785	790	795
Asp Ser Val Phe Ser Lys Asp Ser His Gly Leu Ile Glu Val Ser	800	805	810
Leu Tyr Gln Ile Phe Phe Leu Phe Phe Phe Asn Cys Ser Val Ser	815	820	825
Gln Ala Gly Val Gln Arg Tyr Asp His Ser Ser Leu Arg Pro Gln	830	835	840
Thr Pro Arg Leu Lys Gln Leu Ser His Leu Cys Leu Arg Cys Asn	845	850	855

Arg	Asp	Tyr	Arg	Cys	Lys	Pro	Pro	Thr	Val	Cys	Leu	Ser	Ile	Tyr	
				860					865					870	
Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Leu	Leu	
				875					880					885	
Ser	Cys	Thr	Asp	Gly	Ser	Leu	Thr	Pro	Val	Ile	Pro	Val	Leu	Trp	
				890					895					900	
Glu	Ala	Glu	Ala	Gly	Gly	Ser	Pro	Glu	Val	Gly	Ser	Leu	Arg	Pro	
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Ala

<210> 391

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

tccgtctctg tgaaccgccc cac 23

<210> 392

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

ctcgggcgca ttgtcgttct ggtc 24

<210> 393

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

ccgactgtga aagagaacgc cccagatcca ctgtgtcccc 40

<210> 394

<211> 999

<212> DNA

<213> Homo sapiens

<400> 394

cccaggctct agtgcaggag gagaaggagg aggagcagga ggtggagatt 50

cccagttaaa aggtccaga atcgtgtacc aggagagaa ctgaagtact 100

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<210> 395

<211> 260

<212> PRT

<213> Homo sapiens

<400> 395

Met	Gly	Arg	Pro	Arg	Pro	Arg	Ala	Ala	Lys	Thr	Trp	Met	Phe	Leu
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Leu	Leu	Leu	Gly	Gly	Ala	Trp	Ala	Gly	His	Ser	Arg	Ala	Gln	Glu
			20						25					30

Asp	Lys	Val	Leu	Gly	Gly	His	Glu	Cys	Gln	Pro	His	Ser	Gln	Pro
				35					40					45

Trp	Gln	Ala	Ala	Leu	Phe	Gln	Gly	Gln	Gln	Leu	Leu	Cys	Gly	Gly
				50					55					60

Val	Leu	Val	Gly	Gly	Asn	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Lys
				65					70					75

Lys	Pro	Lys	Tyr	Thr	Val	Arg	Leu	Gly	Asp	His	Ser	Leu	Gln	Asn	80	85	90
Lys	Asp	Gly	Pro	Glu	Gln	Glu	Ile	Pro	Val	Val	Gln	Ser	Ile	Pro	95	100	105
His	Pro	Cys	Tyr	Asn	Ser	Ser	Asp	Val	Glu	Asp	His	Asn	His	Asp	110	115	120
Leu	Met	Leu	Leu	Gln	Leu	Arg	Asp	Gln	Ala	Ser	Leu	Gly	Ser	Lys	125	130	135
Val	Lys	Pro	Ile	Ser	Leu	Ala	Asp	His	Cys	Thr	Gln	Pro	Gly	Gln	140	145	150
Lys	Cys	Thr	Val	Ser	Gly	Trp	Gly	Thr	Val	Thr	Ser	Pro	Arg	Glu	155	160	165
Asn	Phe	Pro	Asp	Thr	Leu	Asn	Cys	Ala	Glu	Val	Lys	Ile	Phe	Pro	170	175	180
Gln	Lys	Lys	Cys	Glu	Asp	Ala	Tyr	Pro	Gly	Gln	Ile	Thr	Asp	Gly	185	190	195
Met	Val	Cys	Ala	Gly	Ser	Ser	Lys	Gly	Ala	Asp	Thr	Cys	Gln	Gly	200	205	210
Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asp	Gly	Ala	Leu	Gln	Gly	Ile	215	220	225
Thr	Ser	Trp	Gly	Ser	Asp	Pro	Cys	Gly	Arg	Ser	Asp	Lys	Pro	Gly	230	235	240
Val	Tyr	Thr	Asn	Ile	Cys	Arg	Tyr	Leu	Asp	Trp	Ile	Lys	Lys	Ile	245	250	255
Ile	Gly	Ser	Lys	Gly											260		

<210> 396

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 396

cagcctacag aataaagatg gccc 24

<210> 397

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 397

ggtgcaatga tctgccaggc tgat 24

<210> 398

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

agaaatacct gtggttcagt ccatcccaaa cccctgctac aacagcag 48

<210> 399

<211> 2236

<212> DNA

<213> Homo sapiens

<400> 399

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cgccgcgagg ccccgcccc gcccgcccc gccccgccc ggccggcggg 200  
ggaaccgggc ggattcctcg cggtcaaac cacctgatcc cataaaacat 250  
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gccgccctcg cctgtgcgc cctgcgcgcc ctgcgcaccc gcggcccag 350  
cccagccaga gccgggaggga gcggagcgcg ccgagcctcg tcccgcggcc 400  
gggcccgggc cgggcccgtag cggcgggccc tggatgcgga cccggccgcg 450  
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ttacaggggt cggcggcagc gtttggtcca gaacgccgc tcccaccag 2150  
atcgcggtat atagagatat gcattttatt ttacttgtgt aaaaatatcg 2200  
gacgacgtgg aataaagagc tcttttctta aaaaaa 2236

<210> 400

<211> 473

<212> PRT  
<213> Homo sapiens

<400> 400

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Leu	Trp	Leu	Gln	Ala	Trp	Gln	Val	Ala	Ala	Pro	Cys	Pro	Gly	Ala	
			20						25					30	
Cys	Val	Cys	Tyr	Asn	Glu	Pro	Lys	Val	Thr	Thr	Ser	Cys	Pro	Gln	
				35					40					45	
Gln	Gly	Leu	Gln	Ala	Val	Pro	Val	Gly	Ile	Pro	Ala	Ala	Ser	Gln	
			50						55					60	
Arg	Ile	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	His	Val	Pro	Ala	Ala	
				65					70					75	
Ser	Phe	Arg	Ala	Cys	Arg	Asn	Leu	Thr	Ile	Leu	Trp	Leu	His	Ser	
				80					85					90	
Asn	Val	Leu	Ala	Arg	Ile	Asp	Ala	Ala	Ala	Phe	Thr	Gly	Leu	Ala	
			95						100					105	
Leu	Leu	Glu	Gln	Leu	Asp	Leu	Ser	Asp	Asn	Ala	Gln	Leu	Arg	Ser	
			110						115					120	
Val	Asp	Pro	Ala	Thr	Phe	His	Gly	Leu	Gly	Arg	Leu	His	Thr	Leu	
			125						130					135	
His	Leu	Asp	Arg	Cys	Gly	Leu	Gln	Glu	Leu	Gly	Pro	Gly	Leu	Phe	
			140						145					150	
Arg	Gly	Leu	Ala	Ala	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	Ala	
			155						160					165	
Leu	Gln	Ala	Leu	Pro	Asp	Asp	Thr	Phe	Arg	Asp	Leu	Gly	Asn	Leu	
			170						175					180	
Thr	His	Leu	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	Ser	Val	Pro	Glu	
			185						190					195	
Arg	Ala	Phe	Arg	Gly	Leu	His	Ser	Leu	Asp	Arg	Leu	Leu	Leu	His	
			200						205					210	
Gln	Asn	Arg	Val	Ala	His	Val	His	Pro	His	Ala	Phe	Arg	Asp	Leu	
			215						220					225	
Gly	Arg	Leu	Met	Thr	Leu	Tyr	Leu	Phe	Ala	Asn	Asn	Leu	Ser	Ala	
			230						235					240	
Leu	Pro	Thr	Glu	Ala	Leu	Ala	Pro	Leu	Arg	Ala	Leu	Gln	Tyr	Leu	
			245						250					255	
Arg	Leu	Asn	Asp	Asn	Pro	Trp	Val	Cys	Asp	Cys	Arg	Ala	Arg	Pro	
			260						265					270	

Leu Trp Ala Trp	Leu Gln Lys Phe Arg Gly Ser Ser Ser Glu Val	
275	280	285
Pro Cys Ser Leu	Pro Gln Arg Leu Ala Gly Arg Asp Leu Lys Arg	
290	295	300
Leu Ala Ala Asn Asp	Leu Gln Gly Cys Ala Val Ala Thr Gly Pro	
305	310	315
Tyr His Pro Ile Trp	Thr Gly Arg Ala Thr Asp Glu Glu Pro Leu	
320	325	330
Gly Leu Pro Lys Cys	Cys Gln Pro Asp Ala Ala Asp Lys Ala Ser	
335	340	345
Val Leu Glu Pro Gly	Arg Pro Ala Ser Ala Gly Asn Ala Leu Lys	
350	355	360
Gly Arg Val Pro Pro	Gly Asp Ser Pro Pro Gly Asn Gly Ser Gly	
365	370	375
Pro Arg His Ile Asn	Asp Ser Pro Phe Gly Thr Leu Pro Gly Ser	
380	385	390
Ala Glu Pro Pro Leu	Thr Ala Val Arg Pro Glu Gly Ser Glu Pro	
395	400	405
Pro Gly Phe Pro Thr	Ser Gly Pro Arg Arg Arg Pro Gly Cys Ser	
410	415	420
Arg Lys Asn Arg Thr	Arg Ser His Cys Arg Leu Gly Gln Ala Gly	
425	430	435
Ser Gly Gly Gly Gly	Thr Gly Asp Ser Glu Gly Ser Gly Ala Leu	
440	445	450
Pro Ser Leu Thr Cys	Ser Leu Thr Pro Leu Gly Leu Ala Leu Val	
455	460	465
Leu Trp Thr Val Leu	Gly Pro Cys	
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<210> 401

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 401

tggtgccct gcagtacctc tacc 24

<210> 402

<211> 24

<212> DNA



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 402

ccctgcaggt cattggcagc tagg 24

<210> 403

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

aggcactgcc tgatgacacc ttccgcgacc tgggcaacct cacac 45

<210> 404

<211> 2738

<212> DNA

<213> Homo sapiens

<400> 404

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agcctcagat actggggact ttacagtccc acagaaccgt cctcccagga 150  
agctgaatcc agcaagaaca atggaggcca gcgggaagct catttgcaga 200  
caaaggcaag tccttttttc ctttctcctt ttgggcttat ctctggcggg 250  
cgcggcggaa cctagaagct attctgtggt ggaggaaact gagggcagct 300  
cctttgtcac caatttagca aaggacctgg gtctggagca gagggaattc 350  
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 tgttttaaag tgaacattta cctttattcc tggttctt 2738

<210> 405  
 <211> 798  
 <212> PRT  
 <213> Homo sapiens

<400> 405  
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 Pro Arg Ser Tyr Ser Val Val Glu Glu Thr Glu Gly Ser Ser Phe  
 35 40 45  
 Val Thr Asn Leu Ala Lys Asp Leu Gly Leu Glu Gln Arg Glu Phe  
 50 55 60  
 Ser Arg Arg Gly Val Arg Val Val Ser Arg Gly Asn Lys Leu His  
 65 70 75  
 Leu Gln Leu Asn Gln Glu Thr Ala Asp Leu Leu Leu Asn Glu Lys  
 80 85 90  
 Leu Asp Arg Glu Asp Leu Cys Gly His Thr Glu Pro Cys Val Leu  
 95 100 105  
 Arg Phe Gln Val Leu Leu Glu Ser Pro Phe Glu Phe Phe Gln Ala  
 110 115 120  
 Glu Leu Gln Val Ile Asp Ile Asn Asp His Ser Pro Val Phe Leu  
 125 130 135  
 Asp Lys Gln Met Leu Val Lys Val Ser Glu Ser Ser Pro Pro Gly  
 140 145 150

Thr Thr Phe Pro	Leu Lys Asn Ala Glu Asp Leu Asp Val Gly Gln	155	160	165
Asn Asn Ile Glu	Asn Tyr Ile Ile Ser Pro Asn Ser Tyr Phe Arg	170	175	180
Val Leu Thr Arg	Lys Arg Ser Asp Gly Arg Lys Tyr Pro Glu Leu	185	190	195
Val Leu Asp Lys	Ala Leu Asp Arg Glu Glu Glu Ala Glu Leu Arg	200	205	210
Leu Thr Leu Thr	Ala Leu Asp Gly Gly Ser Pro Pro Arg Ser Gly	215	220	225
Thr Ala Gln Val	Tyr Ile Glu Val Leu Asp Val Asn Asp Asn Ala	230	235	240
Pro Glu Phe Glu	Gln Pro Phe Tyr Arg Val Gln Ile Ser Glu Asp	245	250	255
Ser Pro Val Gly	Phe Leu Val Val Lys Val Ser Ala Thr Asp Val	260	265	270
Asp Thr Gly Val	Asn Gly Glu Ile Ser Tyr Ser Leu Phe Gln Ala	275	280	285
Ser Glu Glu Ile	Gly Lys Thr Phe Lys Ile Asn Pro Leu Thr Gly	290	295	300
Glu Ile Glu Leu	Lys Lys Gln Leu Asp Phe Glu Lys Leu Gln Ser	305	310	315
Tyr Glu Val Asn	Ile Glu Ala Arg Asp Ala Gly Thr Phe Ser Gly	320	325	330
Lys Cys Thr Val	Leu Ile Gln Val Ile Asp Val Asn Asp His Ala	335	340	345
Pro Glu Val Thr	Met Ser Ala Phe Thr Ser Pro Ile Pro Glu Asn	350	355	360
Ala Pro Glu Thr	Val Val Ala Leu Phe Ser Val Ser Asp Leu Asp	365	370	375
Ser Gly Glu Asn	Gly Lys Ile Ser Cys Ser Ile Gln Glu Asp Leu	380	385	390
Pro Phe Leu Leu	Lys Ser Ala Glu Asn Phe Tyr Thr Leu Leu Thr	395	400	405
Glu Arg Pro Leu	Asp Arg Glu Ser Arg Ala Glu Tyr Asn Ile Thr	410	415	420
Ile Thr Val Thr	Asp Leu Gly Thr Pro Met Leu Ile Thr Gln Leu	425	430	435

Asn Met Thr Val	Leu Ile Ala Asp Val	Asn Asp Asn Ala Pro	Ala
440	445	450	
Phe Thr Gln Thr	Ser Tyr Thr Leu Phe	Val Arg Glu Asn Asn	Ser
455	460	465	
Pro Ala Leu His	Ile Arg Ser Val Ser	Ala Thr Asp Arg Asp	Ser
470	475	480	
Gly Thr Asn Ala	Gln Val Thr Tyr Ser	Leu Leu Pro Pro Gln	Asp
485	490	495	
Pro His Leu Pro	Leu Thr Ser Leu Val	Ser Ile Asn Ala Asp	Asn
500	505	510	
Gly His Leu Phe	Ala Leu Arg Ser Leu	Asp Tyr Glu Ala Leu	Gln
515	520	525	
Gly Phe Gln Phe	Arg Val Gly Ala Ser	Asp His Gly Ser Pro	Ala
530	535	540	
Leu Ser Ser Glu	Ala Leu Val Arg Val	Val Val Leu Asp Ala	Asn
545	550	555	
Asp Asn Ser Pro	Phe Val Leu Tyr Pro	Leu Gln Asn Gly Ser	Ala
560	565	570	
Pro Cys Thr Glu	Leu Val Pro Arg Ala	Ala Glu Pro Gly Tyr	Leu
575	580	585	
Val Thr Lys Val	Val Ala Val Asp Gly	Asp Ser Gly Gln Asn	Ala
590	595	600	
Trp Leu Ser Tyr	Gln Leu Leu Lys Ala	Thr Glu Leu Gly Leu	Phe
605	610	615	
Gly Val Trp Ala	His Asn Gly Glu Val	Arg Thr Ala Arg Leu	Leu
620	625	630	
Ser Glu Arg Asp	Ala Ala Lys His Arg	Leu Val Val Leu Val	Lys
635	640	645	
Asp Asn Gly Glu	Pro Pro Arg Ser Ala	Thr Ala Thr Leu His	Val
650	655	660	
Leu Leu Val Asp	Gly Phe Ser Gln Pro	Tyr Leu Pro Leu Pro	Glu
665	670	675	
Ala Ala Pro Thr	Gln Ala Gln Ala Asp	Leu Leu Thr Val Tyr	Leu
680	685	690	
Val Val Ala Leu	Ala Ser Val Ser Ser	Leu Phe Leu Phe Ser	Val
695	700	705	
Leu Leu Phe Val	Ala Val Arg Leu Cys	Arg Arg Ser Arg Ala	Ala
710	715	720	

Ser Val Gly Arg Cys Leu Val Pro Glu Gly Pro Leu Pro Gly His  
725 730 735

Leu Val Asp Met Ser Gly Thr Arg Thr Leu Ser Gln Ser Tyr Gln  
740 745 750

Tyr Glu Val Cys Leu Ala Gly Gly Ser Gly Thr Asn Glu Phe Lys  
755 760 765

Phe Leu Lys Pro Ile Ile Pro Asn Phe Pro Pro Gln Cys Pro Gly  
770 775 780

Lys Glu Ile Gln Gly Asn Ser Thr Phe Pro Asn Asn Phe Gly Phe  
785 790 795

Asn Ile Gln

<210> 406

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 406

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<210> 407

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 407

agcgttgctca ttgacatcgg cg 22

<210> 408

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 408

ttagttgctc cattcaggag gatctaccct tcctcctgaa atccgcggaa 50

<210> 409

<211> 1379

<212> DNA

<213> Homo sapiens

<400> 409

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 cggtcgacga ccgccccgcg tcatgcggt cctcggtgg tggcaagtat 150  
 tgctgtgggt gctgggactt cccgtccgcg gcgtggaggt tgcagaggaa 200  
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 gatcacatgg tgatgctgtc tgtgattcct ggggaagctg aggacaaagt 400  
 gagttcagag cctagcggcg tcacctgtgg tgctggagga gcggaggact 450  
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 cacttcctg acagagaaga ggagtattac acagagccag aagtggcgga 550  
 atctgacgca gccccgacag aggactcaa taacactgaa agtctgaaat 600  
 ccccaaaggt gaactgtgag gagagaaaca ttacaggatt agaaaatttc 650  
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 gctcttcact ttttggcact ggatgcatct cagcacagca gcctttctac 850  
 caggtttggc accgtagctg ttccataatat tttattattt caaggagcta 900  
 aaccaatggc cagatttaat catacagatc gaacactgga aacactgaaa 950  
 atcttcattt ttaatcagac aggtatagaa gccaagaaga atgtggtggt 1000  
 aactcaagcc gaccaaatag gccctcttcc cagcactttg ataaaaagtg 1050  
 tggactggtt gcttgatatt tccttattct ttttaattag ttttattatg 1100  
 tatgctacca ttcgaactga gattattcgg tggctaattc caggacaaga 1150  
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 agtgacgtgt tgacttgaaa cttcaggcag attaaaagaa tcatttggtg 1300  
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<211> 360  
 <212> PRT  
 <213> Homo sapiens

<400> 410

Met	Val	Pro	Ala	Ala	Gly	Arg	Arg	Pro	Pro	Arg	Val	Met	Arg	Leu	1	5	10	15
Leu	Gly	Trp	Trp	Gln	Val	Leu	Leu	Trp	Val	Leu	Gly	Leu	Pro	Val	20	25	30	
Arg	Gly	Val	Glu	Val	Ala	Glu	Glu	Ser	Gly	Arg	Leu	Trp	Ser	Glu	35	40	45	
Glu	Gln	Pro	Ala	His	Pro	Leu	Gln	Val	Gly	Ala	Val	Tyr	Leu	Gly	50	55	60	
Glu	Glu	Glu	Leu	Leu	His	Asp	Pro	Met	Gly	Gln	Asp	Arg	Ala	Ala	65	70	75	
Glu	Glu	Ala	Asn	Ala	Val	Leu	Gly	Leu	Asp	Thr	Gln	Gly	Asp	His	80	85	90	
Met	Val	Met	Leu	Ser	Val	Ile	Pro	Gly	Glu	Ala	Glu	Asp	Lys	Val	95	100	105	
Ser	Ser	Glu	Pro	Ser	Gly	Val	Thr	Cys	Gly	Ala	Gly	Gly	Ala	Glu	110	115	120	
Asp	Ser	Arg	Cys	Asn	Val	Arg	Glu	Ser	Leu	Phe	Ser	Leu	Asp	Gly	125	130	135	
Ala	Gly	Ala	His	Phe	Pro	Asp	Arg	Glu	Glu	Glu	Tyr	Tyr	Thr	Glu	140	145	150	
Pro	Glu	Val	Ala	Glu	Ser	Asp	Ala	Ala	Pro	Thr	Glu	Asp	Ser	Asn	155	160	165	
Asn	Thr	Glu	Ser	Leu	Lys	Ser	Pro	Lys	Val	Asn	Cys	Glu	Glu	Arg	170	175	180	
Asn	Ile	Thr	Gly	Leu	Glu	Asn	Phe	Thr	Leu	Lys	Ile	Leu	Asn	Met	185	190	195	
Ser	Gln	Asp	Leu	Met	Asp	Phe	Leu	Asn	Pro	Asn	Gly	Ser	Asp	Cys	200	205	210	
Thr	Leu	Val	Leu	Phe	Tyr	Thr	Pro	Trp	Cys	Arg	Phe	Ser	Ala	Ser	215	220	225	
Leu	Ala	Pro	His	Phe	Asn	Ser	Leu	Pro	Arg	Ala	Phe	Pro	Ala	Leu	230	235	240	
His	Phe	Leu	Ala	Leu	Asp	Ala	Ser	Gln	His	Ser	Ser	Leu	Ser	Thr	245	250	255	
Arg	Phe	Gly	Thr	Val	Ala	Val	Pro	Asn	Ile	Leu	Leu	Phe	Gln	Gly				



260	265	270
Ala Lys Pro Met	Ala Arg Phe Asn His Thr Asp Arg Thr Leu Glu	
275	280	285
Thr Leu Lys Ile	Phe Ile Phe Asn Gln Thr Gly Ile Glu Ala Lys	
290	295	300
Lys Asn Val Val	Val Thr Gln Ala Asp Gln Ile Gly Pro Leu Pro	
305	310	315
Ser Thr Leu Ile	Lys Ser Val Asp Trp Leu Leu Val Phe Ser Leu	
320	325	330
Phe Phe Leu Ile	Ser Phe Ile Met Tyr Ala Thr Ile Arg Thr Glu	
335	340	345
Ser Ile Arg Trp	Leu Ile Pro Gly Gln Glu Gln Glu His Val Glu	
350	355	360

<210> 411

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 411

cacagagcca gaagtggcgg aatc 24

<210> 412

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 412

ccacatgttc ctgctcttgt cctgg 25

<210> 413

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 413

cggtagtgac tgtactctag tctgtttta caccctgtgg tgccg 45

<210> 414

<211> 1196

<212> DNA

<213> Homo sapiens

<400> 414

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ggctcggcgc gcgggctctt cctctttggc cagcccgact tctcctacaa 150  
gcgcagcaat tgcaagccca tcccggtcaa cctgcagctg tgccacggca 200  
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<210> 415

<211> 295

<212> PRT

<213> Homo sapiens

<400> 415

Met Leu Gln Gly Pro Gly Ser Leu Leu Leu Leu Phe Leu Ala Ser

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His Cys Cys Leu Gly Ser Ala Arg Gly Leu Phe Leu Phe Gly Gln	20	25	30
Pro Asp Phe Ser Tyr Lys Arg Ser Asn Cys Lys Pro Ile Pro Val	35	40	45
Asn Leu Gln Leu Cys His Gly Ile Glu Tyr Gln Asn Met Arg Leu	50	55	60
Pro Asn Leu Leu Gly His Glu Thr Met Lys Glu Val Leu Glu Gln	65	70	75
Ala Gly Ala Trp Ile Pro Leu Val Met Lys Gln Cys His Pro Asp	80	85	90
Thr Lys Lys Phe Leu Cys Ser Leu Phe Ala Pro Val Cys Leu Asp	95	100	105
Asp Leu Asp Glu Thr Ile Gln Pro Cys His Ser Leu Cys Val Gln	110	115	120
Val Lys Asp Arg Cys Ala Pro Val Met Ser Ala Phe Gly Phe Pro	125	130	135
Trp Pro Asp Met Leu Glu Cys Asp Arg Phe Pro Gln Asp Asn Asp	140	145	150
Leu Cys Ile Pro Leu Ala Ser Ser Asp His Leu Leu Pro Ala Thr	155	160	165
Glu Glu Ala Pro Lys Val Cys Glu Ala Cys Lys Asn Lys Asn Asp	170	175	180
Asp Asp Asn Asp Ile Met Glu Thr Leu Cys Lys Asn Asp Phe Ala	185	190	195
Leu Lys Ile Lys Val Lys Glu Ile Thr Tyr Ile Asn Arg Asp Thr	200	205	210
Lys Ile Ile Leu Glu Thr Lys Ser Lys Thr Ile Tyr Lys Leu Asn	215	220	225
Gly Val Ser Glu Arg Asp Leu Lys Lys Ser Val Leu Trp Leu Lys	230	235	240
Asp Ser Leu Gln Cys Thr Cys Glu Glu Met Asn Asp Ile Asn Ala	245	250	255
Pro Tyr Leu Val Met Gly Gln Lys Gln Gly Gly Glu Leu Val Ile	260	265	270
Thr Ser Val Lys Arg Trp Gln Lys Gly Gln Arg Glu Phe Lys Arg	275	280	285
Ile Ser Arg Ser Ile Arg Lys Leu Gln Cys			

<210> 416  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 416  
cctggctcgc tgctgctgct c 21

<210> 417  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 417  
cctcacaggt gcactgcaag ctgtc 25

<210> 418  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 418  
ctcttcctct ttggccagcc cgacttctcc tacaagcgca gaattgc 47

<210> 419  
<211> 1830  
<212> DNA  
<213> Homo sapiens

<400> 419  
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cgctgggtgt tcctgctcgc gatcagcctg ctcaactgct ccaacgccac 150  
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<210> 420  
<211> 560  
<212> PRT  
<213> Homo sapiens

<400> 420

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Ala	Leu	Cys	Ala	Gln	Arg	Gly	His	Arg	Thr	Tyr	Ala	Arg	Arg	Trp	
				20					25					30	
Val	Phe	Leu	Leu	Ala	Ile	Ser	Leu	Leu	Asn	Cys	Ser	Asn	Ala	Thr	
				35					40					45	
Leu	Trp	Leu	Ser	Phe	Ala	Pro	Val	Ala	Asp	Val	Ile	Ala	Glu	Asp	
				50					55					60	
Leu	Val	Leu	Ser	Met	Glu	Gln	Ile	Asn	Trp	Leu	Ser	Leu	Val	Tyr	
				65					70					75	
Leu	Val	Val	Ser	Thr	Pro	Phe	Gly	Val	Ala	Ala	Ile	Trp	Ile	Leu	
				80					85					90	
Asp	Ser	Val	Gly	Leu	Arg	Ala	Ala	Thr	Ile	Leu	Gly	Ala	Trp	Leu	
				95					100					105	
Asn	Phe	Ala	Gly	Ser	Val	Leu	Arg	Met	Val	Pro	Cys	Met	Val	Val	
				110					115					120	
Gly	Thr	Gln	Asn	Pro	Phe	Ala	Phe	Leu	Met	Gly	Gly	Gln	Ser	Leu	
				125					130					135	
Cys	Ala	Leu	Ala	Gln	Ser	Leu	Val	Ile	Phe	Ser	Pro	Ala	Lys	Leu	
				140					145					150	
Ala	Ala	Leu	Trp	Phe	Pro	Glu	His	Gln	Arg	Ala	Thr	Ala	Asn	Met	
				155					160					165	
Leu	Ala	Thr	Met	Ser	Asn	Pro	Leu	Gly	Val	Leu	Val	Ala	Asn	Val	
				170					175					180	
Leu	Ser	Pro	Val	Leu	Val	Lys	Lys	Gly	Glu	Asp	Ile	Pro	Leu	Met	
				185					190					195	
Leu	Gly	Val	Tyr	Thr	Ile	Pro	Ala	Gly	Val	Val	Cys	Leu	Leu	Ser	
				200					205					210	
Thr	Ile	Cys	Leu	Trp	Glu	Ser	Val	Pro	Pro	Thr	Pro	Pro	Ser	Ala	
				215					220					225	
Gly	Ala	Ala	Ser	Ser	Thr	Ser	Glu	Lys	Phe	Leu	Asp	Gly	Leu	Lys	
				230					235					240	
Leu	Gln	Leu	Met	Trp	Asn	Lys	Ala	Tyr	Val	Ile	Leu	Ala	Val	Cys	
				245					250					255	

Leu Gly Gly Met	Ile Gly Ile Ser Ala	Ser Phe Ser Ala	Leu Leu
260	265	270	
Glu Gln Ile Leu	Cys Ala Ser Gly His	Ser Ser Gly Phe	Ser Gly
275	280	285	
Leu Cys Gly Ala	Leu Phe Ile Thr Phe	Gly Ile Leu Gly	Ala Leu
290	295	300	
Ala Leu Gly Pro	Tyr Val Asp Arg Thr	Lys His Phe Thr	Glu Ala
305	310	315	
Thr Lys Ile Gly	Leu Cys Leu Phe Ser	Leu Ala Cys Val	Pro Phe
320	325	330	
Ala Leu Val Ser	Gln Leu Gln Gly Gln	Thr Leu Ala Leu	Ala Ala
335	340	345	
Thr Cys Ser Leu	Leu Gly Leu Phe Gly	Phe Ser Val Gly	Pro Val
350	355	360	
Ala Met Glu Leu	Ala Val Glu Cys Ser	Phe Pro Val Gly	Glu Gly
365	370	375	
Ala Ala Thr Gly	Met Ile Phe Val Leu	Gly Gln Ala Glu	Gly Ile
380	385	390	
Leu Ile Met Leu	Ala Met Thr Ala Leu	Thr Val Arg Arg	Ser Glu
395	400	405	
Pro Ser Leu Ser	Thr Cys Gln Gln Gly	Glu Asp Pro Leu	Asp Trp
410	415	420	
Thr Val Ser Leu	Leu Leu Met Ala Gly	Leu Cys Thr Phe	Phe Ser
425	430	435	
Cys Ile Leu Ala	Val Phe Phe His Thr	Pro Tyr Arg Arg	Leu Gln
440	445	450	
Ala Glu Ser Gly	Glu Pro Pro Ser Thr	Arg Asn Ala Val	Gly Gly
455	460	465	
Ala Asp Ser Gly	Pro Gly Val Asp Arg	Gly Gly Ala Gly	Arg Ala
470	475	480	
Gly Val Leu Gly	Pro Ser Thr Ala Thr	Pro Glu Cys Thr	Ala Arg
485	490	495	
Gly Ala Ser Leu	Glu Asp Pro Arg Gly	Pro Gly Ser Pro	His Pro
500	505	510	
Ala Cys His Arg	Ala Thr Pro Arg Ala	Gln Gly Pro Ala	Ala Thr
515	520	525	
Asp Ala Pro Ser	Arg Pro Gly Arg Leu	Ala Gly Arg Val	Gln Ala
530	535	540	

Ser Arg Phe Ile Asp Pro Ala Gly Ser His Ser Ser Phe Ser Ser  
545 550 555

Pro Trp Val Ile Thr  
560

<210> 421

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 421

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<210> 422

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 422

cgggtcaata aacctggacg cttgg 25

<210> 423

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 423

tatgtggacc ggaccaagca cttcactgag gccaccaaga ttg 43

<210> 424

<211> 4313

<212> DNA

<213> Homo sapiens

<400> 424

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136.1  
 293  
 429 ✓

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<210> 425

<211> 1184

<212> PRT

<213> Homo sapiens

<400> 425

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Thr Val Lys Tyr	Gln Val Ser Glu Glu	Val Pro Ser Gly Thr	Val
35	40		45
Ile Gly Lys Leu	Ser Gln Glu Leu Gly	Arg Glu Glu Arg Arg	Arg
50	55		60
Gln Ala Gly Ala	Ala Phe Gln Val Leu	Gln Leu Pro Gln Ala	Leu
65	70		75
Pro Ile Gln Val	Asp Ser Glu Glu Gly	Leu Leu Ser Thr Gly	Arg
80	85		90
Arg Leu Asp Arg	Glu Gln Leu Cys Arg	Gln Trp Asp Pro Cys	Leu
95	100		105
Val Ser Phe Asp	Val Leu Ala Thr Gly	Asp Leu Ala Leu Ile	His
110	115		120
Val Glu Ile Gln	Val Leu Asp Ile Asn	Asp His Gln Pro Arg	Phe
125	130		135
Pro Lys Gly Glu	Gln Glu Leu Glu Ile	Ser Glu Ser Ala Ser	Leu
140	145		150
Arg Thr Arg Ile	Pro Leu Asp Arg Ala	Leu Asp Pro Asp Thr	Gly
155	160		165
Pro Asn Thr Leu	His Thr Tyr Thr Leu	Ser Pro Ser Glu His	Phe
170	175		180
Ala Leu Asp Val	Ile Val Gly Pro Asp	Glu Thr Lys His Ala	Glu
185	190		195
Leu Ile Val Val	Lys Glu Leu Asp Arg	Glu Ile His Ser Phe	Phe
200	205		210
Asp Leu Val Leu	Thr Ala Tyr Asp Asn	Gly Asn Pro Pro Lys	Ser
215	220		225
Gly Thr Ser Leu	Val Lys Val Asn Val	Leu Asp Ser Asn Asp	Asn
230	235		240
Ser Pro Ala Phe	Ala Glu Ser Ser Leu	Ala Leu Glu Ile Gln	Glu
245	250		255
Asp Ala Ala Pro	Gly Thr Leu Leu Ile	Lys Leu Thr Ala Thr	Asp
260	265		270
Pro Asp Gln Gly	Pro Asn Gly Glu Val	Glu Phe Phe Leu Ser	Lys
275	280		285
His Met Pro Pro	Glu Val Leu Asp Thr	Phe Ser Ile Asp Ala	Lys
290	295		300

Thr Gly Gln Val	Ile Leu Arg Arg Pro	Leu Asp Tyr Glu Lys Asn
305		310 315
Pro Ala Tyr Glu	Val Asp Val Gln Ala Arg Asp Leu Gly Pro Asn	
320		325 330
Pro Ile Pro Ala	His Cys Lys Val Leu Ile Lys Val Leu Asp Val	
335		340 345
Asn Asp Asn Ile	Pro Ser Ile His Val Thr Trp Ala Ser Gln Pro	
350		355 360
Ser Leu Val Ser	Glu Ala Leu Pro Lys Asp Ser Phe Ile Ala Leu	
365		370 375
Val Met Ala Asp	Asp Leu Asp Ser Gly His Asn Gly Leu Val His	
380		385 390
Cys Trp Leu Ser	Gln Glu Leu Gly His Phe Arg Leu Lys Arg Thr	
395		400 405
Asn Gly Asn Thr	Tyr Met Leu Leu Thr Asn Ala Thr Leu Asp Arg	
410		415 420
Glu Gln Trp Pro	Lys Tyr Thr Leu Thr Leu Leu Ala Gln Asp Gln	
425		430 435
Gly Leu Gln Pro	Leu Ser Ala Lys Lys Gln Leu Ser Ile Gln Ile	
440		445 450
Ser Asp Ile Asn	Asp Asn Ala Pro Val Phe Glu Lys Ser Arg Tyr	
455		460 465
Glu Val Ser Thr	Arg Glu Asn Asn Leu Pro Ser Leu His Leu Ile	
470		475 480
Thr Ile Lys Ala	His Asp Ala Asp Leu Gly Ile Asn Gly Lys Val	
485		490 495
Ser Tyr Arg Ile	Gln Asp Ser Pro Val Ala His Leu Val Ala Ile	
500		505 510
Asp Ser Asn Thr	Gly Glu Val Thr Ala Gln Arg Ser Leu Asn Tyr	
515		520 525
Glu Glu Met Ala	Gly Phe Glu Phe Gln Val Ile Ala Glu Asp Ser	
530		535 540
Gly Gln Pro Met	Leu Ala Ser Ser Val Ser Val Trp Val Ser Leu	
545		550 555
Leu Asp Ala Asn	Asp Asn Ala Pro Glu Val Val Gln Pro Val Leu	
560		565 570
Ser Asp Gly Lys	Ala Ser Leu Ser Val Leu Val Asn Ala Ser Thr	
575		580 585

Gly His Leu Leu Val	Pro Ile Glu Thr	Pro Asn Gly Leu Gly	Pro
590		595	600
Ala Gly Thr Asp Thr	Pro Pro Leu Ala	Thr His Ser Ser Arg	Pro
605		610	615
Phe Leu Leu Thr Thr	Ile Val Ala Arg	Asp Ala Asp Ser Gly	Ala
620		625	630
Asn Gly Glu Pro Leu	Tyr Ser Ile Arg	Asn Gly Asn Glu Ala	His
635		640	645
Leu Phe Ile Leu Asn	Pro His Thr Gly	Gln Leu Phe Val Asn	Val
650		655	660
Thr Asn Ala Ser Ser	Leu Ile Gly Ser	Glu Trp Glu Leu Glu	Ile
665		670	675
Val Val Glu Asp Gln	Gly Ser Pro Pro	Leu Gln Thr Arg Ala	Leu
680		685	690
Leu Arg Val Met Phe	Val Thr Ser Val	Asp His Leu Arg Asp	Ser
695		700	705
Ala Arg Lys Pro Gly	Ala Leu Ser Met	Ser Met Leu Thr Val	Ile
710		715	720
Cys Leu Ala Val Leu	Leu Gly Ile Phe	Gly Leu Ile Leu Ala	Leu
725		730	735
Phe Met Ser Ile Cys	Arg Thr Glu Lys	Lys Asp Asn Arg Ala	Tyr
740		745	750
Asn Cys Arg Glu Ala	Glu Ser Thr Tyr	Arg Gln Gln Pro Lys	Arg
755		760	765
Pro Gln Lys His Ile	Gln Lys Ala Asp	Ile His Leu Val Pro	Val
770		775	780
Leu Arg Gly Gln Ala	Gly Glu Pro Cys	Glu Val Gly Gln Ser	His
785		790	795
Lys Asp Val Asp Lys	Glu Ala Met Met	Glu Ala Gly Trp Asp	Pro
800		805	810
Cys Leu Gln Ala Pro	Phe His Leu Thr	Pro Thr Leu Tyr Arg	Thr
815		820	825
Leu Arg Asn Gln Gly	Asn Gln Gly Ala	Pro Ala Glu Ser Arg	Glu
830		835	840
Val Leu Gln Asp Thr	Val Asn Leu Leu	Phe Asn His Pro Arg	Gln
845		850	855
Arg Asn Ala Ser Arg	Glu Asn Leu Asn	Leu Pro Glu Pro Gln	Pro
860		865	870

Ala Thr Gly Gln Pro Arg Ser Arg Pro Leu Lys Val Ala Gly Ser	875	880	885
Pro Thr Gly Arg Leu Ala Gly Asp Gln Gly Ser Glu Glu Ala Pro	890	895	900
Gln Arg Pro Pro Ala Ser Ser Ala Thr Leu Arg Arg Gln Arg His	905	910	915
Leu Asn Gly Lys Val Ser Pro Glu Lys Glu Ser Gly Pro Arg Gln	920	925	930
Ile Leu Arg Ser Leu Val Arg Leu Ser Val Ala Ala Phe Ala Glu	935	940	945
Arg Asn Pro Val Glu Glu Leu Thr Val Asp Ser Pro Pro Val Gln	950	955	960
Gln Ile Ser Gln Leu Leu Ser Leu Leu His Gln Gly Gln Phe Gln	965	970	975
Pro Lys Pro Asn His Arg Gly Asn Lys Tyr Leu Ala Lys Pro Gly	980	985	990
Gly Ser Arg Ser Ala Ile Pro Asp Thr Asp Gly Pro Ser Ala Arg	995	1000	1005
Ala Gly Gly Gln Thr Asp Pro Glu Gln Glu Glu Gly Pro Leu Asp	1010	1015	1020
Pro Glu Glu Asp Leu Ser Val Lys Gln Leu Leu Glu Glu Glu Leu	1025	1030	1035
Ser Ser Leu Leu Asp Pro Ser Thr Gly Leu Ala Leu Asp Arg Leu	1040	1045	1050
Ser Ala Pro Asp Pro Ala Trp Met Ala Arg Leu Ser Leu Pro Leu	1055	1060	1065
Thr Thr Asn Tyr Arg Asp Asn Val Ile Ser Pro Asp Ala Ala Ala	1070	1075	1080
Thr Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Ala Glu Ala	1085	1090	1095
Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val	1100	1105	1110
Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser	1115	1120	1125
Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser	1130	1135	1140
Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala	1145	1150	1155

Ser Gly Met Lys Val Gln Gly Asp Pro Gly Gly Lys Thr Gly Thr  
1160 1165 1170

Glu Gly Lys Ser Arg Gly Ser Ser Ser Ser Arg Cys Leu  
1175 1180

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 426

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<210> 427

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 427

gtgacgtgga tgcttgggat gttg 24

<210> 428

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 428

tggacacctt cagtattgat gccaagacag gccaggtcat tctgcgtcga 50

<210> 429

<211> 2037

<212> DNA

<213> Homo sapiens

<400> 429

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ggcctcgggg agtgggaagt ggaggcagga gccttcctta cacttcgcca 150

tgagtttcct catcgactcc agcatcatga ttacctcca gatactat 200

tttggatttg ggtggctttt cttcatgcgc caattgttta aagactatga 250

gatacgtcag tatgttgtag aggtgatctt ctccgtgacg tttgcatttt 300



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 ccgccatggc ccaacttggt tattgcagct tataatg 2037

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 <211> 455  
 <212> PRT  
 <213> Homo sapiens

<400> 430

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Leu	Phe	Phe	Gly	Phe	Gly	Trp	Leu	Phe	Phe	Met	Arg	Gln	Leu	Phe
				20					25					30
Lys	Asp	Tyr	Glu	Ile	Arg	Gln	Tyr	Val	Val	Gln	Val	Ile	Phe	Ser
				35					40					45
Val	Thr	Phe	Ala	Phe	Ser	Cys	Thr	Met	Phe	Glu	Leu	Ile	Ile	Phe
				50					55					60
Glu	Ile	Leu	Gly	Val	Leu	Asn	Ser	Ser	Ser	Arg	Tyr	Phe	His	Trp
				65					70					75
Lys	Met	Asn	Leu	Cys	Val	Ile	Leu	Leu	Ile	Leu	Val	Phe	Met	Val
				80					85					90
Pro	Phe	Tyr	Ile	Gly	Tyr	Phe	Ile	Val	Ser	Asn	Ile	Arg	Leu	Leu
				95					100					105
His	Lys	Gln	Arg	Leu	Leu	Phe	Ser	Cys	Leu	Leu	Trp	Leu	Thr	Phe
				110					115					120
Met	Tyr	Phe	Phe	Trp	Lys	Leu	Gly	Asp	Pro	Phe	Pro	Ile	Leu	Ser
				125					130					135
Pro	Lys	His	Gly	Ile	Leu	Ser	Ile	Glu	Gln	Leu	Ile	Ser	Arg	Val
				140					145					150
Gly	Val	Ile	Gly	Val	Thr	Leu	Met	Ala	Leu	Leu	Ser	Gly	Phe	Gly
				155					160					165
Ala	Val	Asn	Cys	Pro	Tyr	Thr	Tyr	Met	Ser	Tyr	Phe	Leu	Arg	Asn
				170					175					180
Val	Thr	Asp	Thr	Asp	Ile	Leu	Ala	Leu	Glu	Arg	Arg	Leu	Leu	Gln

185					190					195				
Thr	Met	Asp	Met	Ile	Ile	Ser	Lys	Lys	Lys	Arg	Met	Ala	Met	Ala
				200					205					210
Arg	Arg	Thr	Met	Phe	Gln	Lys	Gly	Glu	Val	His	Asn	Lys	Pro	Ser
				215					220					225
Gly	Phe	Trp	Gly	Met	Ile	Lys	Ser	Val	Thr	Thr	Ser	Ala	Ser	Gly
				230					235					240
Ser	Glu	Asn	Leu	Thr	Leu	Ile	Gln	Gln	Glu	Val	Asp	Ala	Leu	Glu
				245					250					255
Glu	Leu	Ser	Arg	Gln	Leu	Phe	Leu	Glu	Thr	Ala	Asp	Leu	Tyr	Ala
				260					265					270
Thr	Lys	Glu	Arg	Ile	Glu	Tyr	Ser	Lys	Thr	Phe	Lys	Gly	Lys	Tyr
				275					280					285
Phe	Asn	Phe	Leu	Gly	Tyr	Phe	Phe	Ser	Ile	Tyr	Cys	Val	Trp	Lys
				290					295					300
Ile	Phe	Met	Ala	Thr	Ile	Asn	Ile	Val	Phe	Asp	Arg	Val	Gly	Lys
				305					310					315
Thr	Asp	Pro	Val	Thr	Arg	Gly	Ile	Glu	Ile	Thr	Val	Asn	Tyr	Leu
				320					325					330
Gly	Ile	Gln	Phe	Asp	Val	Lys	Phe	Trp	Ser	Gln	His	Ile	Ser	Phe
				335					340					345
Ile	Leu	Val	Gly	Ile	Ile	Ile	Val	Thr	Ser	Ile	Arg	Gly	Leu	Leu
				350					355					360
Ile	Thr	Leu	Thr	Lys	Phe	Phe	Tyr	Ala	Ile	Ser	Ser	Ser	Lys	Ser
				365					370					375
Ser	Asn	Val	Ile	Val	Leu	Leu	Leu	Ala	Gln	Ile	Met	Gly	Met	Tyr
				380					385					390
Phe	Val	Ser	Ser	Val	Leu	Leu	Ile	Arg	Met	Ser	Met	Pro	Leu	Glu
				395					400					405
Tyr	Arg	Thr	Ile	Ile	Thr	Glu	Val	Leu	Gly	Glu	Leu	Gln	Phe	Asn
				410					415					420
Phe	Tyr	His	Arg	Trp	Phe	Asp	Val	Ile	Phe	Leu	Val	Ser	Ala	Leu
				425					430					435
Ser	Ser	Ile	Leu	Phe	Leu	Tyr	Leu	Ala	His	Lys	Gln	Ala	Pro	Glu
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Lys	Gln	Met	Ala	Pro										
				455										

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<212> DNA  
<213> Homo sapiens

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<221> unsure  
<222> 78, 81, 113, 157, 224, 297  
<223> unknown base

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tggcttttct tcngcgccaa tgtttaaaga ctatgagata cgtcagtatg 150  
ttgtacnggt gatcttctcc gtgacgtttg ccatttcttg caccatgttt 200  
gagctcatca tctttgaaat cttnggagta ttgaatagca gctcccgta 250  
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<210> 432  
<211> 457  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 31, 66, 81-82, 84, 122, 184, 187, 232, 241, 400, 424, 427, 434  
<223> unknown base

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cattttcttg caccatgttt gagctcatca tntttgaaat nttaggagta 250  
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tctgctgac ctggttttca tggtgccctt ttacattggc tattttattg 350  
tgagcaatat ccgactactg cataaacaac gactgctttt ttctgtctn 400  
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cattctc 457

<210> 433

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 433

aagtggagcc ggagccttcc 20

<210> 434

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 434

tcgttggtta tgcagtagtc gg 22

<210> 435

<211> 41

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 435

attgtttaaa gactatgaga tacgtcagta tgttgtagag g 41

<210> 436

<211> 3951

<212> DNA

<213> Homo sapiens

<400> 436

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ttctcacggg ctgtcgcctt caatctggac gtgatgggtg ccttgcgcaa 150

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<210> 437

<211> 1141

<212> PRT

<213> Homo sapiens

<400> 437

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Cys	Tyr	Leu	Phe	Gly	Ser	Leu	Leu	Val	Glu	Leu	Leu	Phe	Ser	Arg
				20					25					30

Ala	Val	Ala	Phe	Asn	Leu	Asp	Val	Met	Gly	Ala	Leu	Arg	Lys	Glu
				35					40					45

Gly	Glu	Pro	Gly	Ser	Leu	Phe	Gly	Phe	Ser	Val	Ala	Leu	His	Arg
				50					55					60

Gln	Leu	Gln	Pro	Arg	Pro	Gln	Ser	Trp	Leu	Leu	Val	Gly	Ala	Pro
				65					70					75

Gln	Ala	Leu	Ala	Leu	Pro	Gly	Gln	Gln	Ala	Asn	Arg	Thr	Gly	Gly
				80					85					90

Leu	Phe	Ala	Cys	Pro	Leu	Ser	Leu	Glu	Glu	Thr	Asp	Cys	Tyr	Arg
				95					100					105



Val Asp Ile Asp	Gln Gly Ala Asp Met	Gln Lys Glu Ser Lys	Glu
110	115		120
Asn Gln Trp Leu	Gly Val Ser Val Arg	Ser Gln Gly Pro Gly	Gly
125	130		135
Lys Ile Val Thr	Cys Ala His Arg Tyr	Glu Ala Arg Gln Arg	Val
140	145		150
Asp Gln Ile Leu	Glu Thr Arg Asp Met	Ile Gly Arg Cys Phe	Val
155	160		165
Leu Ser Gln Asp	Leu Ala Ile Arg Asp	Glu Leu Asp Gly Gly	Glu
170	175		180
Trp Lys Phe Cys	Glu Gly Arg Pro Gln	Gly His Glu Gln Phe	Gly
185	190		195
Phe Cys Gln Gln	Gly Thr Ala Ala Ala	Phe Ser Pro Asp Ser	His
200	205		210
Tyr Leu Leu Phe	Gly Ala Pro Gly Thr	Tyr Asn Trp Lys Gly	Thr
215	220		225
Ala Arg Val Glu	Leu Cys Ala Gln Gly	Ser Ala Asp Leu Ala	His
230	235		240
Leu Asp Asp Gly	Pro Tyr Glu Ala Gly	Gly Glu Lys Glu Gln	Asp
245	250		255
Pro Arg Leu Ile	Pro Val Pro Ala Asn	Ser Tyr Phe Gly Phe	Ser
260	265		270
Ile Asp Ser Gly	Lys Gly Leu Val Arg	Ala Glu Glu Leu Ser	Phe
275	280		285
Val Ala Gly Ala	Pro Arg Ala Asn His	Lys Gly Ala Val Val	Ile
290	295		300
Leu Arg Lys Asp	Ser Ala Ser Arg Leu	Val Pro Glu Val Met	Leu
305	310		315
Ser Gly Glu Arg	Leu Thr Ser Gly Phe	Gly Tyr Ser Leu Ala	Val
320	325		330
Ala Asp Leu Asn	Ser Asp Gly Trp Pro	Asp Leu Ile Val Gly	Ala
335	340		345
Pro Tyr Phe Phe	Glu Arg Gln Glu Glu	Leu Gly Gly Ala Val	Tyr
350	355		360
Val Tyr Leu Asn	Gln Gly Gly His Trp	Ala Gly Ile Ser Pro	Leu
365	370		375
Arg Leu Cys Gly	Ser Pro Asp Ser Met	Phe Gly Ile Ser Leu	Ala
380	385		390

Val Leu Gly Asp	Leu Asn Gln Asp Gly	Phe Pro Asp Ile Ala	Val
395	400		405
Gly Ala Pro Phe	Asp Gly Asp Gly Lys	Val Phe Ile Tyr His	Gly
410	415		420
Ser Ser Leu Gly	Val Val Ala Lys Pro	Ser Gln Val Leu Glu	Gly
425	430		435
Glu Ala Val Gly	Ile Lys Ser Phe Gly	Tyr Ser Leu Ser Gly	Ser
440	445		450
Leu Asp Met Asp	Gly Asn Gln Tyr Pro	Asp Leu Leu Val Gly	Ser
455	460		465
Leu Ala Asp Thr	Ala Val Leu Phe Arg	Ala Arg Pro Ile Leu	His
470	475		480
Val Ser His Glu	Val Ser Ile Ala Pro	Arg Ser Ile Asp Leu	Glu
485	490		495
Gln Pro Asn Cys	Ala Gly Gly His Ser	Val Cys Val Asp Leu	Arg
500	505		510
Val Cys Phe Ser	Tyr Ile Ala Val Pro	Ser Ser Tyr Ser Pro	Thr
515	520		525
Val Ala Leu Asp	Tyr Val Leu Asp Ala	Asp Thr Asp Arg Arg	Leu
530	535		540
Arg Gly Gln Val	Pro Arg Val Thr Phe	Leu Ser Arg Asn Leu	Glu
545	550		555
Glu Pro Lys His	Gln Ala Ser Gly Thr	Val Trp Leu Lys His	Gln
560	565		570
His Asp Arg Val	Cys Gly Asp Ala Met	Phe Gln Leu Gln Glu	Asn
575	580		585
Val Lys Asp Lys	Leu Arg Ala Ile Val	Val Thr Leu Ser Tyr	Ser
590	595		600
Leu Gln Thr Pro	Arg Leu Arg Arg Gln	Ala Pro Gly Gln Gly	Leu
605	610		615
Pro Pro Val Ala	Pro Ile Leu Asn Ala	His Gln Pro Ser Thr	Gln
620	625		630
Arg Ala Glu Ile	His Phe Leu Lys Gln	Gly Cys Gly Glu Asp	Lys
635	640		645
Ile Cys Gln Ser	Asn Leu Gln Leu Val	His Ala Arg Phe Cys	Thr
650	655		660
Arg Val Ser Asp	Thr Glu Phe Gln Pro	Leu Pro Met Asp Val	Asp
665	670		675

Gly Thr Thr Ala	Leu Phe Ala Leu Ser	Gly Gln Pro Val Ile	Gly
680		685	690
Leu Glu Leu Met	Val Thr Asn Leu Pro	Ser Asp Pro Ala Gln	Pro
695		700	705
Gln Ala Asp Gly	Asp Asp Ala His Glu	Ala Gln Leu Leu Val	Met
710		715	720
Leu Pro Asp Ser	Leu His Tyr Ser Gly	Val Arg Ala Leu Asp	Pro
725		730	735
Ala Glu Lys Pro	Leu Cys Leu Ser Asn	Glu Asn Ala Ser His	Val
740		745	750
Glu Cys Glu Leu	Gly Asn Pro Met Lys	Arg Gly Ala Gln Val	Thr
755		760	765
Phe Tyr Leu Ile	Leu Ser Thr Ser Gly	Ile Ser Ile Glu Thr	Thr
770		775	780
Glu Leu Glu Val	Glu Leu Leu Leu Ala	Thr Ile Ser Glu Gln	Glu
785		790	795
Leu His Pro Val	Ser Ala Arg Ala Arg	Val Phe Ile Glu Leu	Pro
800		805	810
Leu Ser Ile Ala	Gly Met Ala Ile Pro	Gln Gln Leu Phe Phe	Ser
815		820	825
Gly Val Val Arg	Gly Glu Arg Ala Met	Gln Ser Glu Arg Asp	Val
830		835	840
Gly Ser Lys Val	Lys Tyr Glu Val Thr	Val Ser Asn Gln Gly	Gln
845		850	855
Ser Leu Arg Thr	Leu Gly Ser Ala Phe	Leu Asn Ile Met Trp	Pro
860		865	870
His Glu Ile Ala	Asn Gly Lys Trp Leu	Leu Tyr Pro Met Gln	Val
875		880	885
Glu Leu Glu Gly	Gly Gln Gly Pro Gly	Gln Lys Gly Leu Cys	Ser
890		895	900
Pro Arg Pro Asn	Ile Leu His Leu Asp	Val Asp Ser Arg Asp	Arg
905		910	915
Arg Arg Arg Glu	Leu Glu Pro Pro Glu	Gln Gln Glu Pro Gly	Glu
920		925	930
Arg Gln Glu Pro	Ser Met Ser Trp Trp	Pro Val Ser Ser Ala	Glu
935		940	945
Lys Lys Lys Asn	Ile Thr Leu Asp Cys	Ala Arg Gly Thr Ala	Asn
950		955	960

Cys Val Val Phe Ser Cys Pro Leu Tyr Ser Phe Asp Arg Ala Ala	965	970	975
Val Leu His Val Trp Gly Arg Leu Trp Asn Ser Thr Phe Leu Glu	980	985	990
Glu Tyr Ser Ala Val Lys Ser Leu Glu Val Ile Val Arg Ala Asn	995	1000	1005
Ile Thr Val Lys Ser Ser Ile Lys Asn Leu Met Leu Arg Asp Ala	1010	1015	1020
Ser Thr Val Ile Pro Val Met Val Tyr Leu Asp Pro Met Ala Val	1025	1030	1035
Val Ala Glu Gly Val Pro Trp Trp Val Ile Leu Leu Ala Val Leu	1040	1045	1050
Ala Gly Leu Leu Val Leu Ala Leu Leu Val Leu Leu Leu Trp Lys	1055	1060	1065
Met Gly Phe Phe Lys Arg Ala Lys His Pro Glu Ala Thr Val Pro	1070	1075	1080
Gln Tyr His Ala Val Lys Ile Pro Arg Glu Asp Arg Gln Gln Phe	1085	1090	1095
Lys Glu Glu Lys Thr Gly Thr Ile Leu Arg Asn Asn Trp Gly Ser	1100	1105	1110
Pro Arg Arg Glu Gly Pro Asp Ala His Pro Ile Leu Ala Ala Asp	1115	1120	1125
Gly His Pro Glu Leu Gly Pro Asp Gly His Pro Gly Pro Gly Thr	1130	1135	1140

Ala

<210> 438

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 438

ggctgacacc gcagtgtctt tcag 24

<210> 439

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 439.

gctgctgggg actgcaatgt agct 24

<210> 440

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 440

catcctccat gtctcccatg aggtctctat tgctccacga agcatc 46

<210> 441

<211> 1964

<212> DNA

<213> Homo sapiens

<400> 441

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ggagctgcga gcacagtgtt ggctcacaac aagatgtctc aggtgtcagc 150  
cgtactgtgt gtgtgtgcag ccgcttggtg cagtcagtct ctcgcagctg 200  
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aagcagtgcc cagtggctta tcccagccct gtttgtggtt cagatggtca 600  
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<210> 442

<211> 436

<212> PRT

<213> Homo sapiens

<400> 442

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Cys	Ser	Gln	Ser	Leu	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ala	Ala	Gly
				20					25					30

Gly Arg Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu

	35		40		45
Thr Thr Ile Ser	Gln Tyr Asp Lys Glu	Val Gly Gln Trp Asn Lys			
	50	55		60	
Phe Arg Asp Glu	Val Glu Asp Asp Tyr	Phe Arg Thr Trp Ser Pro			
	65	70		75	
Gly Lys Pro Phe	Asp Gln Ala Leu Asp	Pro Ala Lys Asp Pro Cys			
	80	85		90	
Leu Lys Met Lys	Cys Ser Arg His Lys	Val Cys Ile Ala Gln Asp			
	95	100		105	
Ser Gln Thr Ala	Val Cys Ile Ser His	Arg Arg Leu Thr His Arg			
	110	115		120	
Met Lys Glu Ala	Gly Val Asp His Arg	Gln Trp Arg Gly Pro Ile			
	125	130		135	
Leu Ser Thr Cys	Lys Gln Cys Pro Val	Val Tyr Pro Ser Pro Val			
	140	145		150	
Cys Gly Ser Asp	Gly His Thr Tyr Ser	Phe Gln Cys Lys Leu Glu			
	155	160		165	
Tyr Gln Ala Cys	Val Leu Gly Lys Gln	Ile Ser Val Lys Cys Glu			
	170	175		180	
Gly His Cys Pro	Cys Pro Ser Asp Lys	Pro Thr Ser Thr Ser Arg			
	185	190		195	
Asn Val Lys Arg	Ala Cys Ser Asp Leu	Glu Phe Arg Glu Val Ala			
	200	205		210	
Asn Arg Leu Arg	Asp Trp Phe Lys Ala	Leu His Glu Ser Gly Ser			
	215	220		225	
Gln Asn Lys Lys	Thr Lys Thr Leu Leu	Arg Pro Glu Arg Ser Arg			
	230	235		240	
Phe Asp Thr Ser	Ile Leu Pro Ile Cys	Lys Asp Ser Leu Gly Trp			
	245	250		255	
Met Phe Asn Arg	Leu Asp Thr Asn Tyr	Asp Leu Leu Leu Asp Gln			
	260	265		270	
Ser Glu Leu Arg	Ser Ile Tyr Leu Asp	Lys Asn Glu Gln Cys Thr			
	275	280		285	
Lys Ala Phe Phe	Asn Ser Cys Asp Thr	Tyr Lys Asp Ser Leu Ile			
	290	295		300	
Ser Asn Asn Glu	Trp Cys Tyr Cys Phe	Gln Arg Gln Gln Asp Pro			
	305	310		315	
Pro Cys Gln Thr	Glu Leu Ser Asn Ile	Gln Lys Arg Gln Gly Val			

320										325					330				
Lys	Lys	Leu	Leu	Gly	Gln	Tyr	Ile	Pro	Leu	Cys	Asp	Glu	Asp	Gly					
				335					340					345					
Tyr	Tyr	Lys	Pro	Thr	Gln	Cys	His	Gly	Ser	Val	Gly	Gln	Cys	Trp					
				350					355					360					
Cys	Val	Asp	Arg	Tyr	Gly	Asn	Glu	Val	Met	Gly	Ser	Arg	Ile	Asn					
				365					370					375					
Gly	Val	Ala	Asp	Cys	Ala	Ile	Asp	Phe	Glu	Ile	Ser	Gly	Asp	Phe					
				380					385					390					
Ala	Ser	Gly	Asp	Phe	His	Glu	Trp	Thr	Asp	Asp	Glu	Asp	Asp	Glu					
				395					400					405					
Asp	Asp	Ile	Met	Asn	Asp	Glu	Asp	Glu	Ile	Glu	Asp	Asp	Asp	Glu					
				410					415					420					
Asp	Glu	Gly	Asp	Asp	Asp	Asp	Gly	Gly	Asp	Asp	His	Asp	Val	Tyr					
				425					430					435					

Ile

<210> 443

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 443

cagcaatatt cagaagcggc aaggg 25

<210> 444

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 444

catcatggtc atcaccacca tcatcatc 28

<210> 445

<211> 48

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 445



ggttactaca agccaacaca atgtcatggc agtgttggac agtgctgg 48

<210> 446

<211> 3617

<212> DNA

<213> Homo sapiens

<400> 446

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gatggagcag gattagatat tgatttccat cttgcctctc cagaaggcaa 350  
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cttaaaaattt ggggtataga acccctcaac aggttagtaa tgctggaatt 2400  
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tagtataaaa agagatacat ttccctctta ggcccctggg agaagagcag 2500  
cttagatttc cctactggca aggtttttta aaatgaggta aatgccgtat 2550  
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<210> 447

<211> 229

<212> PRT

<213> Homo sapiens

<400> 447

Met	Gly	Asp	Lys	Ile	Trp	Leu	Pro	Phe	Pro	Val	Leu	Leu	Leu	Ala
1				5					10					15

Ala	Leu	Pro	Pro	Val	Leu	Leu	Pro	Gly	Ala	Ala	Gly	Phe	Thr	Pro
				20					25					30

Ser	Leu	Asp	Ser	Asp	Phe	Thr	Phe	Thr	Leu	Pro	Ala	Gly	Gln	Lys
				35					40					45

Glu	Cys	Phe	Tyr	Gln	Pro	Met	Pro	Leu	Lys	Ala	Ser	Leu	Glu	Ile
				50					55					60

Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His	65	70	75
Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe Glu Gln Arg Lys	80	85	90
Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly Asp Tyr Met	95	100	105
Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys Val Ile	110	115	120
Phe Phe Glu Leu Ile Leu Asp Asn Met Gly Glu Gln Ala Gln Glu	125	130	135
Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp	140	145	150
Met Lys Leu Glu Asp Ile Leu Glu Ser Ile Asn Ser Ile Lys Ser	155	160	165
Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu Leu Arg Ala Phe	170	175	180
Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe Asp Arg Val	185	190	195
Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val Val Ser	200	205	210
Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys Arg	215	220	225

Lys Ser Arg Thr

<210> 448

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 448

cccagcaggg ctgggcgaca aga 23

<210> 449

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 449

gtcttccagt ttcatatcca ata 23

<210> 450

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 450

ccagaaggag cacggggaag ggcagccaga tcttgctgcc cat 43

<210> 451

<211> 859

<212> DNA

<213> Homo sapiens

<400> 451

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agcataccag atctcaccag agagtcgcag aactatgct gcctcccatg 100

gccctgccca gtgtgtcctg gatgctgctt tcttgctca ttctcctgtg 150

tcaggttcaa ggtgaagaaa ccagaagga actgccctct ccacggatca 200

gtgtgccaa aggtccaag gcctatggct cccctgcta tgccttgttt 250

ttgtcaccaa aatcctggat ggatgcagat ctggcttgcc agaagcggcc 300

ctctggaaaa ctggtgtctg tgctcagtgg ggctgaggga tccttcgtgt 350

cctccctggg gaggagcatt agtaacagct actcatacat ctggattggg 400

ctccatgacc ccacacaggg ctctgagcct gatggagatg gatgggagtg 450

gagtagcact gatgtgatga attactttgc atgggagaaa aatccctcca 500

ccatcttaaa ccctggccac tgtgggagcc tgtcaagaag cacaggattt 550

ctgaagtgga aagattataa ctgtgatgca aagttaccct atgtctgcaa 600

gttcaaggac tagggcaggt ggaagtcag cagcctcagc ttggcgtgca 650

gctcatcatg gacatgagac cagtgtgaag actcaccctg gaagagaata 700

tttcccccaa actgccctac ctgactacct tgcatgatc ctccttcttt 750

ttcctttttc ttcaccttca tttcaggctt ttctctgtct tccatgtctt 800

gagatctcag agaataataa taaaaatgtt actttataaa aaaaaaaaaa 850

aaaaaaaaa 859

<210> 452

<211> 175

<212> PRT  
<213> Homo sapiens

<400> 452

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Ser	Cys	Leu	Ile	Leu	Leu	Cys	Gln	Val	Gln	Gly	Glu	Glu	Thr	Gln	
				20					25					30	
Lys	Glu	Leu	Pro	Ser	Pro	Arg	Ile	Ser	Cys	Pro	Lys	Gly	Ser	Lys	
				35					40					45	
Ala	Tyr	Gly	Ser	Pro	Cys	Tyr	Ala	Leu	Phe	Leu	Ser	Pro	Lys	Ser	
				50					55					60	
Trp	Met	Asp	Ala	Asp	Leu	Ala	Cys	Gln	Lys	Arg	Pro	Ser	Gly	Lys	
				65					70					75	
Leu	Val	Ser	Val	Leu	Ser	Gly	Ala	Glu	Gly	Ser	Phe	Val	Ser	Ser	
				80					85					90	
Leu	Val	Arg	Ser	Ile	Ser	Asn	Ser	Tyr	Ser	Tyr	Ile	Trp	Ile	Gly	
				95					100					105	
Leu	His	Asp	Pro	Thr	Gln	Gly	Ser	Glu	Pro	Asp	Gly	Asp	Gly	Trp	
				110					115					120	
Glu	Trp	Ser	Ser	Thr	Asp	Val	Met	Asn	Tyr	Phe	Ala	Trp	Glu	Lys	
				125					130					135	
Asn	Pro	Ser	Thr	Ile	Leu	Asn	Pro	Gly	His	Cys	Gly	Ser	Leu	Ser	
				140					145					150	
Arg	Ser	Thr	Gly	Phe	Leu	Lys	Trp	Lys	Asp	Tyr	Asn	Cys	Asp	Ala	
				155					160					165	
Lys	Leu	Pro	Tyr	Val	Cys	Lys	Phe	Lys	Asp						
				170					175						

<210> 453  
<211> 550  
<212> DNA  
<213> Homo sapiens

<400> 453

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ggcgtcctg gcgtgggtgc tggctgcctg cggagagctg gcgccggccc 150  
tgcgctgcta cgtctgtccg gagccacag gagtgtcggg ctgtgtcacc 200  
atcgccacct gcaccaccaa cgaaaccatg tgcaagacca cactctactc 250  
ccgggagata gtgtaccct tccaggggga ctccacggtg accaagtcct 300

gtgccagcaa gtgtaagccc tcggatgtgg atggcatcgg ccagaccctg 350  
cccgtgtcct gctgcaatac tgagctgtgc aatgtagacg gggcgcccgc 400  
tctgaacagc ctccactgcg gggccctcac gctcctccca ctcttgagcc 450  
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cgaatgcctt gaagaagtgc cccctgcacc aggaaaaaaaa aaaaaaaaaa 550

<210> 454  
<211> 125  
<212> PRT  
<213> Homo sapiens

<400> 454  
Met Arg Gly Thr Arg Leu Ala Leu Leu Ala Leu Val Leu Ala Ala  
1 5 10 15  
Cys Gly Glu Leu Ala Pro Ala Leu Arg Cys Tyr Val Cys Pro Glu  
20 25 30  
Pro Thr Gly Val Ser Asp Cys Val Thr Ile Ala Thr Cys Thr Thr  
35 40 45  
Asn Glu Thr Met Cys Lys Thr Thr Leu Tyr Ser Arg Glu Ile Val  
50 55 60  
Tyr Pro Phe Gln Gly Asp Ser Thr Val Thr Lys Ser Cys Ala Ser  
65 70 75  
Lys Cys Lys Pro Ser Asp Val Asp Gly Ile Gly Gln Thr Leu Pro  
80 85 90  
Val Ser Cys Cys Asn Thr Glu Leu Cys Asn Val Asp Gly Ala Pro  
95 100 105  
Ala Leu Asn Ser Leu His Cys Gly Ala Leu Thr Leu Leu Pro Leu  
110 115 120  
Leu Ser Leu Arg Leu  
125

<210> 455  
<211> 1518  
<212> DNA  
<213> Homo sapiens

<400> 455  
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attttctctt tctttctccc tcttgagtcc ttctgagatg atggctctgg 150  
gcgcagcggg agctacccgg gtctttgtcg cgatggtagc ggcggctctc 200

ggcgccacc ctctgctggg agtgagcgcc accttgaact cggttctcaa 250  
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 aataagtacc agaccattga caactaccag ccgtacccgt gcgcagagga 400  
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 tgtgtcttct gatcaaaatc atttccgagg agaaattgag gaaaccatca 600  
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 aagcatagga gaaaaggctc tcatggacta gaaatattcc agcgttggtta 850  
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 gtaattcttc taggcttcac acttgtcaga gacactaaac cagctatcca 950  
 aatgcagtga actcctttta tataatagat gctatgaaaa ccttttatga 1000  
 ccttcatcaa ctcaatccta aggatataca agttctgtgg tttcagttaa 1050  
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 ttatggaact cccctgtgat tgcagtaaata tactgtattg taaattctca 1150  
 gtgtggcact tacctgtaaa tgcaatgaaa cttttaatta tttttctaaa 1200  
 ggtgctgcac tgcctatttt tcctcttggt atgtaaattt ttgtacacat 1250  
 tgattgttat cttgactgac aaatattcta tattgaactg aagtaaataca 1300  
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 gagtctagaa cgcaaggatc tcttggaatg acaaatgata ggtacctaaa 1400  
 atgtaacatg aaaatactag cttattttct gaaatgtact atcttaatgc 1450  
 ttaaattata tttcccttta ggctgtgata gtttttgaaa taaaatttaa 1500  
 catttaaaaa aaaaaaaaa 1518

<210> 456

<211> 266



<212> PRT

<213> Homo sapiens

<400> 456

Met	Met	Ala	Leu	Gly	Ala	Ala	Gly	Ala	Thr	Arg	Val	Phe	Val	Ala	
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Met	Val	Ala	Ala	Ala	Leu	Gly	Gly	His	Pro	Leu	Leu	Gly	Val	Ser	
				20					25					30	
Ala	Thr	Leu	Asn	Ser	Val	Leu	Asn	Ser	Asn	Ala	Ile	Lys	Asn	Leu	
				35					40					45	
Pro	Pro	Pro	Leu	Gly	Gly	Ala	Ala	Gly	His	Pro	Gly	Ser	Ala	Val	
				50					55					60	
Ser	Ala	Ala	Pro	Gly	Ile	Leu	Tyr	Pro	Gly	Gly	Asn	Lys	Tyr	Gln	
				65					70					75	
Thr	Ile	Asp	Asn	Tyr	Gln	Pro	Tyr	Pro	Cys	Ala	Glu	Asp	Glu	Glu	
				80					85					90	
Cys	Gly	Thr	Asp	Glu	Tyr	Cys	Ala	Ser	Pro	Thr	Arg	Gly	Gly	Asp	
				95					100					105	
Ala	Gly	Val	Gln	Ile	Cys	Leu	Ala	Cys	Arg	Lys	Arg	Arg	Lys	Arg	
				110					115					120	
Cys	Met	Arg	His	Ala	Met	Cys	Cys	Pro	Gly	Asn	Tyr	Cys	Lys	Asn	
				125					130					135	
Gly	Ile	Cys	Val	Ser	Ser	Asp	Gln	Asn	His	Phe	Arg	Gly	Glu	Ile	
				140					145					150	
Glu	Glu	Thr	Ile	Thr	Glu	Ser	Phe	Gly	Asn	Asp	His	Ser	Thr	Leu	
				155					160					165	
Asp	Gly	Tyr	Ser	Arg	Arg	Thr	Thr	Leu	Ser	Ser	Lys	Met	Tyr	His	
				170					175					180	
Thr	Lys	Gly	Gln	Glu	Gly	Ser	Val	Cys	Leu	Arg	Ser	Ser	Asp	Cys	
				185					190					195	
Ala	Ser	Gly	Leu	Cys	Cys	Ala	Arg	His	Phe	Trp	Ser	Lys	Ile	Cys	
				200					205					210	
Lys	Pro	Val	Leu	Lys	Glu	Gly	Gln	Val	Cys	Thr	Lys	His	Arg	Arg	
				215					220					225	
Lys	Gly	Ser	His	Gly	Leu	Glu	Ile	Phe	Gln	Arg	Cys	Tyr	Cys	Gly	
				230					235					240	
Glu	Gly	Leu	Ser	Cys	Arg	Ile	Gln	Lys	Asp	His	His	Gln	Ala	Ser	
				245					250					255	
Asn	Ser	Ser	Arg	Leu	His	Thr	Cys	Gln	Arg	His					
				260					265						

<210> 457  
<211> 638  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 30, 123, 133, 139, 180, 214, 259, 282, 308, 452, 467, 471, 473,  
509, 556  
<223> unknown base

<400> 457  
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catttttttt tctttctcct tcnggagtc tnttgagang atggtttttg 150  
gcgcagcggg agctaaccgc gttttttgtn gcgatggtag cggcggtttt 200  
cggcggccac ctnttgctgg gagtgagcgc caccttgaat cggttttcaa 250  
ttccaacgnt atcaagaacc tgccccacc gntgggcggc gctgcggggc 300  
accaggntt tgcagtcagc gccgcgccg gaatcctgta cccgggcggg 350  
aataagtacc agaccattga caattaccag ccgtaccgt gcgcagagga 400  
cgaggagtgc ggcactgatg agtactgcgc tagtcccacc cgcggagggg 450  
angcgggcgt gcaaantgt ntngcctgca ggaagcgccg aaaacgctgc 500  
atgcgtcang ctatgtgctg ccccggaat tactgcaaaa atggaatatg 550  
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<210> 458  
<211> 4040  
<212> DNA  
<213> Homo sapiens

<400> 458  
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ttctctcctg cacgcggtgc ttgggctcgg ccaggcgggg tccgccgcca 150  
gggtttgagg atgggggagt agctacagga agcgaccccg cgatggcaag 200  
gtatatTTTT gtggaatgaa aaggaagtat tagaaatgag ctgaagacca 250  
ttcacagatt aatatttttg gggacagatt tgtgatgctt gattcacct 300

tgaagtaatg tagacagaag ttctcaaatt tgcatattac atcaactgga 350  
accagcagtg aatcttaatg ttcacttaaa tcagaacttg cataagaaag 400  
agaatgggag tctgggttaa taaagatgac tatatcagag acttgaaaaag 450  
gatcattctc tgttttctga tagtgtatat ggccatttta gtgggcacag 500  
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ggagaaaagg gacttgagga taatcaagggt ggccagtatg aaagctggaa 750  
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 caagtatata aatctaggaa agggatcttc tagtttctgt gttgtttaga 3900  
 ctcaaagaat cacaaatttg tcagtaacat gtagttgttt agttataatt 3950  
 cagagtgtac agaatggtaa aaattccaat cagtcaaaag aggtcaatga 4000  
 attaaaaggc ttgcaacttt ttcaaaaaaa aaaaaaaaaa 4040

<210> 459

<211> 747

<212> PRT

<213> Homo sapiens

<400> 459

Met	Gly	Val	Trp	Leu	Asn	Lys	Asp	Asp	Tyr	Ile	Arg	Asp	Leu	Lys
1				5					10				15	

Arg	Ile	Ile	Leu	Cys	Phe	Leu	Ile	Val	Tyr	Met	Ala	Ile	Leu	Val
			20						25				30	

Gly	Thr	Asp	Gln	Asp	Phe	Tyr	Ser	Leu	Leu	Gly	Val	Ser	Lys	Thr
			35						40				45	

Ala	Ser	Ser	Arg	Glu	Ile	Arg	Gln	Ala	Phe	Lys	Lys	Leu	Ala	Leu
			50						55				60	

Lys	Leu	His	Pro	Asp	Lys	Asn	Pro	Asn	Asn	Pro	Asn	Ala	His	Gly
			65						70				75	

Asp Phe Leu Lys Ile Asn Arg Ala Tyr Glu Val Leu Lys Asp Glu	80	85	90
Asp Leu Arg Lys Lys Tyr Asp Lys Tyr Gly Glu Lys Gly Leu Glu	95	100	105
Asp Asn Gln Gly Gly Gln Tyr Glu Ser Trp Asn Tyr Tyr Arg Tyr	110	115	120
Asp Phe Gly Ile Tyr Asp Asp Asp Pro Glu Ile Ile Thr Leu Glu	125	130	135
Arg Arg Glu Phe Asp Ala Ala Val Asn Ser Gly Glu Leu Trp Phe	140	145	150
Val Asn Phe Tyr Ser Pro Gly Cys Ser His Cys His Asp Leu Ala	155	160	165
Pro Thr Trp Arg Asp Phe Ala Lys Glu Val Asp Gly Leu Leu Arg	170	175	180
Ile Gly Ala Val Asn Cys Gly Asp Asp Arg Met Leu Cys Arg Met	185	190	195
Lys Gly Val Asn Ser Tyr Pro Ser Leu Phe Ile Phe Arg Ser Gly	200	205	210
Met Ala Pro Val Lys Tyr His Gly Asp Arg Ser Lys Glu Ser Leu	215	220	225
Val Ser Phe Ala Met Gln His Val Arg Ser Thr Val Thr Glu Leu	230	235	240
Trp Thr Gly Asn Phe Val Asn Ser Ile Gln Thr Ala Phe Ala Ala	245	250	255
Gly Ile Gly Trp Leu Ile Thr Phe Cys Ser Lys Gly Gly Asp Cys	260	265	270
Leu Thr Ser Gln Thr Arg Leu Arg Leu Ser Gly Met Leu Phe Leu	275	280	285
Asn Ser Leu Asp Ala Lys Glu Ile Tyr Leu Glu Val Ile His Asn	290	295	300
Leu Pro Asp Phe Glu Leu Leu Ser Ala Asn Thr Leu Glu Asp Arg	305	310	315
Leu Ala His His Arg Trp Leu Leu Phe Phe His Phe Gly Lys Asn	320	325	330
Glu Asn Ser Asn Asp Pro Glu Leu Lys Lys Leu Lys Thr Leu Leu	335	340	345
Lys Asn Asp His Ile Gln Val Gly Arg Phe Asp Cys Ser Ser Ala	350	355	360

Pro Asp Ile Cys Ser Asn Leu Tyr Val Phe Gln Pro Ser Leu Ala	365	370	375
Val Phe Lys Gly Gln Gly Thr Lys Glu Tyr Glu Ile His His Gly	380	385	390
Lys Lys Ile Leu Tyr Asp Ile Leu Ala Phe Ala Lys Glu Ser Val	395	400	405
Asn Ser His Val Thr Thr Leu Gly Pro Gln Asn Phe Pro Ala Asn	410	415	420
Asp Lys Glu Pro Trp Leu Val Asp Phe Phe Ala Pro Trp Cys Pro	425	430	435
Pro Cys Arg Ala Leu Leu Pro Glu Leu Arg Arg Ala Ser Asn Leu	440	445	450
Leu Tyr Gly Gln Leu Lys Phe Gly Thr Leu Asp Cys Thr Val His	455	460	465
Glu Gly Leu Cys Asn Met Tyr Asn Ile Gln Ala Tyr Pro Thr Thr	470	475	480
Val Val Phe Asn Gln Ser Asn Ile His Glu Tyr Glu Gly His His	485	490	495
Ser Ala Glu Gln Ile Leu Glu Phe Ile Glu Asp Leu Met Asn Pro	500	505	510
Ser Val Val Ser Leu Thr Pro Thr Thr Phe Asn Glu Leu Val Thr	515	520	525
Gln Arg Lys His Asn Glu Val Trp Met Val Asp Phe Tyr Ser Pro	530	535	540
Trp Cys His Pro Cys Gln Val Leu Met Pro Glu Trp Lys Arg Met	545	550	555
Ala Arg Thr Leu Thr Gly Leu Ile Asn Val Gly Ser Ile Asp Cys	560	565	570
Gln Gln Tyr His Ser Phe Cys Ala Gln Glu Asn Val Gln Arg Tyr	575	580	585
Pro Glu Ile Arg Phe Phe Pro Pro Lys Ser Asn Lys Ala Tyr Gln	590	595	600
Tyr His Ser Tyr Asn Gly Trp Asn Arg Asp Ala Tyr Ser Leu Arg	605	610	615
Ile Trp Gly Leu Gly Phe Leu Pro Gln Val Ser Thr Asp Leu Thr	620	625	630
Pro Gln Thr Phe Ser Glu Lys Val Leu Gln Gly Lys Asn His Trp	635	640	645

Val Ile Asp Phe Tyr Ala Pro Trp Cys Gly Pro Cys Gln Asn Phe  
650 655 660

Ala Pro Glu Phe Glu Leu Leu Ala Arg Met Ile Lys Gly Lys Val  
665 670 675

Lys Ala Gly Lys Val Asp Cys Gln Ala Tyr Ala Gln Thr Cys Gln  
680 685 690

Lys Ala Gly Ile Arg Ala Tyr Pro Thr Val Lys Phe Tyr Phe Tyr  
695 700 705

Glu Arg Ala Lys Arg Asn Phe Gln Glu Glu Gln Ile Asn Thr Arg  
710 715 720

Asp Ala Lys Ala Ile Ala Ala Leu Ile Ser Glu Lys Leu Glu Thr  
725 730 735

Leu Arg Asn Gln Gly Lys Arg Asn Lys Asp Glu Leu  
740 745

<210> 460

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 460

actccccagg ctgttcacac tgcc 24

<210> 461

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 461

gatcagccag ccaataccag cagc 24

<210> 462

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 462

gtggtgatga tagaatgctt tgccgaatga aaggagtcaa cagctatccc 50

<210> 463

<211> 1818

<212> DNA



<213> Homo sapiens

<400> 463

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ggacagagca aagccatgaa catcatccta gaaatccttc tgcttctgat 100  
caccatcatc tactcctact tggagtcggt ggtgaagttt ttcattcctc 150  
agaggagaaa atctgtggct ggggagattg ttctcattac tggagctggg 200  
catggaatag gcaggcagac tacttatgaa ttgcaaaac gacagagcat 250  
attggttctg tgggatatta ataagcgcg tgtggaggaa actgcagctg 300  
agtgccgaaa actaggcgtc actgcgcatg cgtatgtggt agactgcagc 350  
aacagagaag agatctatcg ctctctaaat caggtgaaga aagaagtggg 400  
tgatgtaaca atcgtggtga ataatgctgg gacagtatat ccagccgata 450  
ttctcagcac caaggatgaa gagattacca agacatttga ggtcaacatc 500  
ctaggacatt ttggatcac aaaagcactt cttccatcga tgatggagag 550  
aaatcatggc cacatcgtca cagtggcttc agtgtgcggc cacgaaggga 600  
ttccttacct catcccatat tgttcagca aatttgccgc tgttggcttt 650  
cacagaggtc tgacatcaga acttcaggcc ttgggaaaaa ctggtatcaa 700  
aacctcatgt ctctgccag tttttgtgaa tactgggttc accaaaaatc 750  
caagcacaag attatggcct gtattggaga cagatgaagt cgtaagaagt 800  
ctgatagatg gaatacttac caataagaaa atgatttttg ttccatcgta 850  
tatcaatatc tttctgagac tacagaagtt tcttctgaa cgcgcctcag 900  
cgattttaaa tcgtatgcag aatattcaat ttgaagcagt ggttggccac 950  
aaaatcaaaa tgaaatgaat aaataagctc cagccagaga tgtatgcatg 1000  
ataatgatat gaatagtttc gaatcaatgc tgcaaagctt tatttcacat 1050  
tttttcagtc ctgataatat taaaaacatt ggtttggcac tagcagcagt 1100  
caaacgaaca agattaatta cctgtcttcc tgtttctcaa gaatatttac 1150  
gtagtttttc ataggtctgt ttttccttcc atgcctctta aaaacttctg 1200  
tgcttacata aacatactta aaaggttttc tttaagatat tttatttttc 1250  
catttaaagg tggacaaaag ctacctccct aaaagtaaata acaaagagaa 1300  
cttatttaca caggaaggt ttaagactgt tcaagtagca ttccaatctg 1350

tagccatgcc acagaatatc aacaagaaca cagaatgagt gcacagctaa 1400  
 gagatcaagt ttcagcaggc agctttatct caacctggac atattttaag 1450  
 attcagcatt tgaaagattt ccctagcctc ttcctttttc attagcccaa 1500  
 aacggtgcaa ctctattctg gactttatta cttgattctg tcttctgtat 1550  
 aactctgaag tccaccaaaa gtggaccctc tatatttcct ccctttttat 1600  
 agtcttataa gatacattat gaaaggtgac cgactctatt ttaaattctca 1650  
 gaattttaag ttctagcccc atgataacct ttttctttgt aatttatgct 1700  
 ttcatatatc cttgggtccca gagatgttta gacaatttta ggctcaaaaa 1750  
 ttaaagctaa cacaggaaaa ggaactgtac tggctattac ataagaaaca 1800  
 atggacccaa gagaagaa 1818

<210> 464  
 <211> 300  
 <212> PRT  
 <213> Homo sapiens

<400> 464

Met	Asn	Ile	Ile	Leu	Glu	Ile	Leu	Leu	Leu	Leu	Ile	Thr	Ile	Ile	1	5	10	15
Tyr	Ser	Tyr	Leu	Glu	Ser	Leu	Val	Lys	Phe	Phe	Ile	Pro	Gln	Arg	20	25	30	
Arg	Lys	Ser	Val	Ala	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	35	40	45	
His	Gly	Ile	Gly	Arg	Gln	Thr	Thr	Tyr	Glu	Phe	Ala	Lys	Arg	Gln	50	55	60	
Ser	Ile	Leu	Val	Leu	Trp	Asp	Ile	Asn	Lys	Arg	Gly	Val	Glu	Glu	65	70	75	
Thr	Ala	Ala	Glu	Cys	Arg	Lys	Leu	Gly	Val	Thr	Ala	His	Ala	Tyr	80	85	90	
Val	Val	Asp	Cys	Ser	Asn	Arg	Glu	Glu	Ile	Tyr	Arg	Ser	Leu	Asn	95	100	105	
Gln	Val	Lys	Lys	Glu	Val	Gly	Asp	Val	Thr	Ile	Val	Val	Asn	Asn	110	115	120	
Ala	Gly	Thr	Val	Tyr	Pro	Ala	Asp	Leu	Leu	Ser	Thr	Lys	Asp	Glu	125	130	135	
Glu	Ile	Thr	Lys	Thr	Phe	Glu	Val	Asn	Ile	Leu	Gly	His	Phe	Trp	140	145	150	
Ile	Thr	Lys	Ala	Leu	Leu	Pro	Ser	Met	Met	Glu	Arg	Asn	His	Gly				

155										160				165				
His	Ile	Val	Thr	Val	Ala	Ser	Val	Cys	Gly	His	Glu	Gly	Ile	Pro				
				170					175					180				
Tyr	Leu	Ile	Pro	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala	Val	Gly	Phe				
				185					190					195				
His	Arg	Gly	Leu	Thr	Ser	Glu	Leu	Gln	Ala	Leu	Gly	Lys	Thr	Gly				
				200					205					210				
Ile	Lys	Thr	Ser	Cys	Leu	Cys	Pro	Val	Phe	Val	Asn	Thr	Gly	Phe				
				215					220					225				
Thr	Lys	Asn	Pro	Ser	Thr	Arg	Leu	Trp	Pro	Val	Leu	Glu	Thr	Asp				
				230					235					240				
Glu	Val	Val	Arg	Ser	Leu	Ile	Asp	Gly	Ile	Leu	Thr	Asn	Lys	Lys				
				245					250					255				
Met	Ile	Phe	Val	Pro	Ser	Tyr	Ile	Asn	Ile	Phe	Leu	Arg	Leu	Gln				
				260					265					270				
Lys	Phe	Leu	Pro	Glu	Arg	Ala	Ser	Ala	Ile	Leu	Asn	Arg	Met	Gln				
				275					280					285				
Asn	Ile	Gln	Phe	Glu	Ala	Val	Val	Gly	His	Lys	Ile	Lys	Met	Lys				
				290					295					300				

<210> 465  
 <211> 1547  
 <212> DNA  
 <213> Homo sapiens

<400> 465  
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 gttcccagca ggatgccccg gctctgcagg aagctgaagt gagaggcccg 100  
 gagagggccc agcccgcccc gggcaggatg accaaggccc ggctgttccg 150  
 gctgtggctg gtgctggggg cggtgttcat gatcctgctg atcatcgtgt 200  
 actgggacag cgcaggcgcc gcgcacttct acttgcacac gtccttctct 250  
 aggccgcaca cggggccgcc gctgcccacg cccgggcccg acagggacag 300  
 ggagctcacg gccgactccg atgtcgacga gtttctggac aagtttctca 350  
 gtgctggcgt gaagcagagc gaccttccca gaaaggagac ggagcagccg 400  
 cctgcgccgg ggagcatgga ggagagcgtg agaggctacg actggtcccc 450  
 gcgcgacgcc cggcgcagcc cagaccaggg ccggcagcag gcggagcgga 500  
 ggagcgtgct gcggggcttc tgcgccaact ccagcctggc cttccccacc 550

aaggagcgcg cattcgacga catccccaac tcggagctga gccacctgat 600  
cgtggacgac cggcacgggg ccatctactg ctacgtgccc aaggtggcct 650  
gcaccaactg gaagcgcgtg atgatcgtgc tgagcgggaag cctgctgcac 700  
cgcggtgcg cctaccgcga cccgctgcg atcccgcgcg agcacgtgca 750  
caacgccagc gcgcacctga cttcaacaa gttctggcgc cgctacggga 800  
agctctcccg ccacctcatg aaggtcaagc tcaagaagta caccaagttc 850  
ctcttcgtgc gcgacccctt cgtgcgcctg atctccgcct tccgcagcaa 900  
gttcgagctg gagaacgagg agttctaccg caagttcgcc gtgcccattgc 950  
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ttccgcgctg gcctcaaggt gtccttcgcc aacttcattc agtacctgct 1050  
ggaccgcgac acggagaagc tggcgccctt caacgagcac tggcggcagg 1100  
tgtaccgcct ctgccacccg tgccagatcg actacgactt cgtggggaag 1150  
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ggaccggcag ctccgcttcc ccccgagcta ccggaacagg accgccagca 1250  
gctgggagga ggactgggtc gccaagatcc ccctggcctg gaggcagcag 1300  
ctgtataaac tctacgaggc cgactttgtt ctcttcggct accccaagcc 1350  
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cctggaacct gacgcacgcg cactccagtt ttttatgac ctacgatttt 1450  
gcaatctggg cttctgttc actccactgc ctctatccat tgagtactgt 1500  
atcgatattg tttttaaga ttaatatatt tcaggtattt aatacga 1547

<210> 466

<211> 414

<212> PRT

<213> Homo sapiens

<400> 466

Met	Thr	Lys	Ala	Arg	Leu	Phe	Arg	Leu	Trp	Leu	Val	Leu	Gly	Ser
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Val	Phe	Met	Ile	Leu	Leu	Ile	Ile	Val	Tyr	Trp	Asp	Ser	Ala	Gly
			20						25					30

Ala	Ala	His	Phe	Tyr	Leu	His	Thr	Ser	Phe	Ser	Arg	Pro	His	Thr
			35						40					45

Gly	Pro	Pro	Leu	Pro	Thr	Pro	Gly	Pro	Asp	Arg	Asp	Arg	Glu	Leu
			50						55					60

Thr	Ala	Asp	Ser	Asp	Val	Asp	Glu	Phe	Leu	Asp	Lys	Phe	Leu	Ser		65	70	75
Ala	Gly	Val	Lys	Gln	Ser	Asp	Leu	Pro	Arg	Lys	Glu	Thr	Glu	Gln		80	85	90
Pro	Pro	Ala	Pro	Gly	Ser	Met	Glu	Glu	Ser	Val	Arg	Gly	Tyr	Asp		95	100	105
Trp	Ser	Pro	Arg	Asp	Ala	Arg	Arg	Ser	Pro	Asp	Gln	Gly	Arg	Gln		110	115	120
Gln	Ala	Glu	Arg	Arg	Ser	Val	Leu	Arg	Gly	Phe	Cys	Ala	Asn	Ser		125	130	135
Ser	Leu	Ala	Phe	Pro	Thr	Lys	Glu	Arg	Ala	Phe	Asp	Asp	Ile	Pro		140	145	150
Asn	Ser	Glu	Leu	Ser	His	Leu	Ile	Val	Asp	Asp	Arg	His	Gly	Ala		155	160	165
Ile	Tyr	Cys	Tyr	Val	Pro	Lys	Val	Ala	Cys	Thr	Asn	Trp	Lys	Arg		170	175	180
Val	Met	Ile	Val	Leu	Ser	Gly	Ser	Leu	Leu	His	Arg	Gly	Ala	Pro		185	190	195
Tyr	Arg	Asp	Pro	Leu	Arg	Ile	Pro	Arg	Glu	His	Val	His	Asn	Ala		200	205	210
Ser	Ala	His	Leu	Thr	Phe	Asn	Lys	Phe	Trp	Arg	Arg	Tyr	Gly	Lys		215	220	225
Leu	Ser	Arg	His	Leu	Met	Lys	Val	Lys	Leu	Lys	Lys	Tyr	Thr	Lys		230	235	240
Phe	Leu	Phe	Val	Arg	Asp	Pro	Phe	Val	Arg	Leu	Ile	Ser	Ala	Phe		245	250	255
Arg	Ser	Lys	Phe	Glu	Leu	Glu	Asn	Glu	Glu	Phe	Tyr	Arg	Lys	Phe		260	265	270
Ala	Val	Pro	Met	Leu	Arg	Leu	Tyr	Ala	Asn	His	Thr	Ser	Leu	Pro		275	280	285
Ala	Ser	Ala	Arg	Glu	Ala	Phe	Arg	Ala	Gly	Leu	Lys	Val	Ser	Phe		290	295	300
Ala	Asn	Phe	Ile	Gln	Tyr	Leu	Leu	Asp	Pro	His	Thr	Glu	Lys	Leu		305	310	315
Ala	Pro	Phe	Asn	Glu	His	Trp	Arg	Gln	Val	Tyr	Arg	Leu	Cys	His		320	325	330
Pro	Cys	Gln	Ile	Asp	Tyr	Asp	Phe	Val	Gly	Lys	Leu	Glu	Thr	Leu		335	340	345

Asp	Glu	Asp	Ala	Ala	Gln	Leu	Leu	Gln	Leu	Leu	Gln	Val	Asp	Arg	
				350					355					360	
Gln	Leu	Arg	Phe	Pro	Pro	Ser	Tyr	Arg	Asn	Arg	Thr	Ala	Ser	Ser	
				365					370					375	
Trp	Glu	Glu	Asp	Trp	Phe	Ala	Lys	Ile	Pro	Leu	Ala	Trp	Arg	Gln	
				380					385					390	
Gln	Leu	Tyr	Lys	Leu	Tyr	Glu	Ala	Asp	Phe	Val	Leu	Phe	Gly	Tyr	
				395					400					405	
Pro	Lys	Pro	Glu	Asn	Leu	Leu	Arg	Asp							
				410											

<210> 467  
 <211> 1071  
 <212> DNA  
 <213> Homo sapiens

<400> 467  
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 acgggatggc tacgggaacg cgctatgccg ggaaggtggg ggtcgtgacc 150  
 gggggcgggc gcggcatcgg agctgggatc gtgcgcgcct tcgtgaacag 200  
 cggggcccga gtggttatct gcgacaagga tgagtctggg ggccggggccc 250  
 tggagcagga gctccctgga gctgtcttta tcctctgtga tgtgactcag 300  
 gaagatgatg tgaagaccct ggtttctgag accatccgcc gatttgggccg 350  
 cctggattgt gttgtcaaca acgctggcca ccacccaccc ccacagaggc 400  
 ctgaggagac ctctgcccag ggattccgcc agctgctgga gctgaaccta 450  
 ctggggacgt acaccttgac caagctcgcc ctcccctacc tgcggaagag 500  
 tcaagggaat gtcataca tctccagcct ggtgggggca atcgccagg 550  
 cccaggcagt tccctatgtg gccaccaagg gggcagtaac agccatgacc 600  
 aaagctttgg ccctggatga aagtccatat ggtgtccgag tcaactgtat 650  
 ctccccagga aacatctgga ccccgtgtg ggaggagctg gcagccttaa 700  
 tgccagaccc tagggccaca atccgagagg gcatgctggc ccagccactg 750  
 ggccgcatgg gccagcccgc tgaggctggg gctgcggcag tgttcttggc 800  
 ctccgaagcc aacttctgca cgggcattga actgctcgtg acgggggggtg 850  
 cagagctggg gtacgggtgc aaggccagtc ggagcacccc cgtggacgcc 900

cccgatatcc cttcctgatt tctctcattt ctacttgggg cccccttcct 950  
 aggactctcc caccctcaaac tccaacctgt atcagatgca gcccctcaagc 1000  
 ccttagactc taagcccagt tagcaagggtg ccgggtcacc ctgcagggtc 1050  
 ccataaaaac gatttgcagc c 1071

<210> 468  
 <211> 270  
 <212> PRT  
 <213> Homo sapiens

<400> 468

Met	Ala	Thr	Gly	Thr	Arg	Tyr	Ala	Gly	Lys	Val	Val	Val	Val	Thr	1	5	10	15
Gly	Gly	Gly	Arg	Gly	Ile	Gly	Ala	Gly	Ile	Val	Arg	Ala	Phe	Val	20	25	30	
Asn	Ser	Gly	Ala	Arg	Val	Val	Ile	Cys	Asp	Lys	Asp	Glu	Ser	Gly	35	40	45	
Gly	Arg	Ala	Leu	Glu	Gln	Glu	Leu	Pro	Gly	Ala	Val	Phe	Ile	Leu	50	55	60	
Cys	Asp	Val	Thr	Gln	Glu	Asp	Asp	Val	Lys	Thr	Leu	Val	Ser	Glu	65	70	75	
Thr	Ile	Arg	Arg	Phe	Gly	Arg	Leu	Asp	Cys	Val	Val	Asn	Asn	Ala	80	85	90	
Gly	His	His	Pro	Pro	Pro	Gln	Arg	Pro	Glu	Glu	Thr	Ser	Ala	Gln	95	100	105	
Gly	Phe	Arg	Gln	Leu	Leu	Glu	Leu	Asn	Leu	Leu	Gly	Thr	Tyr	Thr	110	115	120	
Leu	Thr	Lys	Leu	Ala	Leu	Pro	Tyr	Leu	Arg	Lys	Ser	Gln	Gly	Asn	125	130	135	
Val	Ile	Asn	Ile	Ser	Ser	Leu	Val	Gly	Ala	Ile	Gly	Gln	Ala	Gln	140	145	150	
Ala	Val	Pro	Tyr	Val	Ala	Thr	Lys	Gly	Ala	Val	Thr	Ala	Met	Thr	155	160	165	
Lys	Ala	Leu	Ala	Leu	Asp	Glu	Ser	Pro	Tyr	Gly	Val	Arg	Val	Asn	170	175	180	
Cys	Ile	Ser	Pro	Gly	Asn	Ile	Trp	Thr	Pro	Leu	Trp	Glu	Glu	Leu	185	190	195	
Ala	Ala	Leu	Met	Pro	Asp	Pro	Arg	Ala	Thr	Ile	Arg	Glu	Gly	Met	200	205	210	

Leu	Ala	Gln	Pro	Leu	Gly	Arg	Met	Gly	Gln	Pro	Ala	Glu	Val	Gly
				215					220					225
Ala	Ala	Ala	Val	Phe	Leu	Ala	Ser	Glu	Ala	Asn	Phe	Cys	Thr	Gly
				230					235					240
Ile	Glu	Leu	Leu	Val	Thr	Gly	Gly	Ala	Glu	Leu	Gly	Tyr	Gly	Cys
				245					250					255
Lys	Ala	Ser	Arg	Ser	Thr	Pro	Val	Asp	Ala	Pro	Asp	Ile	Pro	Ser
				260					265					270

<210> 469  
 <211> 687  
 <212> DNA  
 <213> Homo sapiens

<400> 469  
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 cctcacaacc tgctgtttct tcttaccatt tccatcttcc tggggctggg 100  
 ccagcccagg agccccaaaa gcaagaggaa ggggcaagg cggcctgggc 150  
 ccctggcccc tggccctcac caggtgccac tggacctggt gtcacgcatg 200  
 aaaccgtatg cccgcatgga ggagtatgag aggaacatcg aggagatggt 250  
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Gly	Gln	Gly	Arg	Pro	Gly	Pro	Leu	Ala	Pro	Gly	Pro	His	Gln	Val
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Pro	Leu	Asp	Leu	Val	Ser	Arg	Met	Lys	Pro	Tyr	Ala	Arg	Met	Glu
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Glu	Tyr	Glu	Arg	Asn	Ile	Glu	Glu	Met	Val	Ala	Gln	Leu	Arg	Asn
				65					70					75
Ser	Ser	Glu	Leu	Ala	Gln	Arg	Lys	Cys	Glu	Val	Asn	Leu	Gln	Leu
				80					85					90
Trp	Met	Ser	Asn	Lys	Arg	Ser	Leu	Ser	Pro	Trp	Gly	Tyr	Ser	Ile
				95					100					105
Asn	His	Asp	Pro	Ser	Arg	Ile	Pro	Val	Asp	Leu	Pro	Glu	Ala	Arg
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Cys	Leu	Cys	Leu	Gly	Cys	Val	Asn	Pro	Phe	Thr	Met	Gln	Glu	Asp
				125					130					135
Arg	Ser	Met	Val	Ser	Val	Pro	Val	Phe	Ser	Gln	Val	Pro	Val	Arg
				140					145					150
Arg	Arg	Leu	Cys	Pro	Pro	Pro	Pro	Arg	Thr	Gly	Pro	Cys	Arg	Gln
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Arg	Ala	Val	Met	Glu	Thr	Ile	Ala	Val	Gly	Cys	Thr	Cys	Ile	Phe
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<211> 2368

<212> DNA

<213> Homo sapiens

<400> 471

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 Ala Pro Trp Cys Pro Ser Cys Gln Gln Thr Asp Ser Glu Trp Glu  
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 Ala Phe Ala Lys Asn Gly Glu Ile Leu Gln Ile Ser Val Gly Lys  
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 Val Asp Val Ile Gln Glu Pro Gly Leu Ser Gly Arg Phe Phe Val  
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 Thr Thr Leu Pro Ala Phe Phe His Ala Lys Asp Gly Ile Phe Arg  
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 Arg Tyr Arg Gly Pro Gly Ile Phe Glu Asp Leu Gln Asn Tyr Ile  
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Ile Ser Gly Lys	Ile Trp His Leu His	Asn Tyr Phe Thr Val Thr	170	175	180
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Thr Leu Val Phe	Gly Leu Phe Met Gly	Leu Val Leu Val Val Ile	200	205	210
Ser Glu Cys Phe	Tyr Val Pro Leu Pro	Arg His Leu Ser Glu Arg	215	220	225
Ser Glu Gln Asn	Arg Arg Ser Glu Glu	Ala His Arg Ala Glu Gln	230	235	240
Leu Gln Asp Ala	Glu Glu Glu Lys Asp	Asp Ser Asn Glu Glu Glu	245	250	255
Asn Lys Asp Ser	Leu Val Asp Asp Glu	Glu Glu Lys Glu Asp Leu	260	265	270
Gly Asp Glu Asp	Glu Ala Glu Glu Glu	Glu Glu Glu Asp Asn Leu	275	280	285
Ala Ala Gly Val	Asp Glu Glu Arg Ser	Glu Ala Asn Asp Gln Gly	290	295	300
Pro Pro Gly Glu	Asp Gly Val Thr Arg	Glu Glu Val Glu Pro Glu	305	310	315
Glu Ala Glu Glu	Gly Ile Ser Glu Gln	Pro Cys Pro Ala Asp Thr	320	325	330
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<213> Artificial Sequence

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<212> DNA

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<223> Synthetic oligonucleotide probe

<400> 474

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<211> 2478

<212> DNA

<213> Homo sapiens

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<400> 477

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Val	Ser	Glu	Lys	Gly	Ser	Cys	Ala	Ala	Ser	Pro	Pro	Trp	Arg	Leu	35	40	45	
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<210> 483

<211> 693

<212> PRT

<213> Homo sapiens

<400> 483

Met	Thr	Pro	Gln	Ser	Leu	Leu	Gln	Thr	Thr	Leu	Phe	Leu	Leu	Ser
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Leu	Leu	Phe	Leu	Val	Gln	Gly	Ala	His	Gly	Arg	Gly	His	Arg	Glu
				20				25						30
Asp	Phe	Arg	Phe	Cys	Ser	Gln	Arg	Asn	Gln	Thr	His	Arg	Ser	Ser
				35				40						45
Leu	His	Tyr	Lys	Pro	Thr	Pro	Asp	Leu	Arg	Ile	Ser	Ile	Glu	Asn
				50				55						60
Ser	Glu	Glu	Ala	Leu	Thr	Val	His	Ala	Pro	Phe	Pro	Ala	Ala	His
				65				70						75
Pro	Ala	Ser	Arg	Ser	Phe	Pro	Asp	Pro	Arg	Gly	Leu	Tyr	His	Phe
				80				85						90

Cys	Leu	Tyr	Trp	Asn	Arg	His	Ala	Gly	Arg	Leu	His	Leu	Leu	Tyr	95	100	105
Gly	Lys	Arg	Asp	Phe	Leu	Leu	Ser	Asp	Lys	Ala	Ser	Ser	Leu	Leu	110	115	120
Cys	Phe	Gln	His	Gln	Glu	Glu	Ser	Leu	Ala	Gln	Gly	Pro	Pro	Leu	125	130	135
Leu	Ala	Thr	Ser	Val	Thr	Ser	Trp	Trp	Ser	Pro	Gln	Asn	Ile	Ser	140	145	150
Leu	Pro	Ser	Ala	Ala	Ser	Phe	Thr	Phe	Ser	Phe	His	Ser	Pro	Pro	155	160	165
His	Thr	Ala	Ala	His	Asn	Ala	Ser	Val	Asp	Met	Cys	Glu	Leu	Lys	170	175	180
Arg	Asp	Leu	Gln	Leu	Leu	Ser	Gln	Phe	Leu	Lys	His	Pro	Gln	Lys	185	190	195
Ala	Ser	Arg	Arg	Pro	Ser	Ala	Ala	Pro	Ala	Ser	Gln	Gln	Leu	Gln	200	205	210
Ser	Leu	Glu	Ser	Lys	Leu	Thr	Ser	Val	Arg	Phe	Met	Gly	Asp	Met	215	220	225
Val	Ser	Phe	Glu	Glu	Asp	Arg	Ile	Asn	Ala	Thr	Val	Trp	Lys	Leu	230	235	240
Gln	Pro	Thr	Ala	Gly	Leu	Gln	Asp	Leu	His	Ile	His	Ser	Arg	Gln	245	250	255
Glu	Glu	Glu	Gln	Ser	Glu	Ile	Met	Glu	Tyr	Ser	Val	Leu	Leu	Pro	260	265	270
Arg	Thr	Leu	Phe	Gln	Arg	Thr	Lys	Gly	Arg	Ser	Gly	Glu	Ala	Glu	275	280	285
Lys	Arg	Leu	Leu	Leu	Val	Asp	Phe	Ser	Ser	Gln	Ala	Leu	Phe	Gln	290	295	300
Asp	Lys	Asn	Ser	Ser	Gln	Val	Leu	Gly	Glu	Lys	Val	Leu	Gly	Ile	305	310	315
Val	Val	Gln	Asn	Thr	Lys	Val	Ala	Asn	Leu	Thr	Glu	Pro	Val	Val	320	325	330
Leu	Thr	Phe	Gln	His	Gln	Leu	Gln	Pro	Lys	Asn	Val	Thr	Leu	Gln	335	340	345
Cys	Val	Phe	Trp	Val	Glu	Asp	Pro	Thr	Leu	Ser	Ser	Pro	Gly	His	350	355	360
Trp	Ser	Ser	Ala	Gly	Cys	Glu	Thr	Val	Arg	Arg	Glu	Thr	Gln	Thr	365	370	375

Ser Cys Phe Cys Asn His Leu Thr Tyr Phe Ala Val Leu Met Val	380	385	390
Ser Ser Val Glu Val Asp Ala Val His Lys His Tyr Leu Ser Leu	395	400	405
Leu Ser Tyr Val Gly Cys Val Val Ser Ala Leu Ala Cys Leu Val	410	415	420
Thr Ile Ala Ala Tyr Leu Cys Ser Arg Val Pro Leu Pro Cys Arg	425	430	435
Arg Lys Pro Arg Asp Tyr Thr Ile Lys Val His Met Asn Leu Leu	440	445	450
Leu Ala Val Phe Leu Leu Asp Thr Ser Phe Leu Leu Ser Glu Pro	455	460	465
Val Ala Leu Thr Gly Ser Glu Ala Gly Cys Arg Ala Ser Ala Ile	470	475	480
Phe Leu His Phe Ser Leu Leu Thr Cys Leu Ser Trp Met Gly Leu	485	490	495
Glu Gly Tyr Asn Leu Tyr Arg Leu Val Val Glu Val Phe Gly Thr	500	505	510
Tyr Val Pro Gly Tyr Leu Leu Lys Leu Ser Ala Met Gly Trp Gly	515	520	525
Phe Pro Ile Phe Leu Val Thr Leu Val Ala Leu Val Asp Val Asp	530	535	540
Asn Tyr Gly Pro Ile Ile Leu Ala Val His Arg Thr Pro Glu Gly	545	550	555
Val Ile Tyr Pro Ser Met Cys Trp Ile Arg Asp Ser Leu Val Ser	560	565	570
Tyr Ile Thr Asn Leu Gly Leu Phe Ser Leu Val Phe Leu Phe Asn	575	580	585
Met Ala Met Leu Ala Thr Met Val Val Gln Ile Leu Arg Leu Arg	590	595	600
Pro His Thr Gln Lys Trp Ser His Val Leu Thr Leu Leu Gly Leu	605	610	615
Ser Leu Val Leu Gly Leu Pro Trp Ala Leu Ile Phe Phe Ser Phe	620	625	630
Ala Ser Gly Thr Phe Gln Leu Val Val Leu Tyr Leu Phe Ser Ile	635	640	645
Ile Thr Ser Phe Gln Gly Phe Leu Ile Phe Ile Trp Tyr Trp Ser	650	655	660

Met Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu Lys Ser Asn  
665 670 675

Ser Asp Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr Ser Ser  
680 685 690

Ser Arg Ile

<210> 484

<211> 516

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 68, 70, 84, 147

<223> unknown base

<400> 484

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cgggtggcct gacaggctct gaaggctggc tgccgagcca gtgccatctt 200  
cctgcacttc tctgtctcac ctgcctttcc tggatggggc tcgaggggta 250  
caacctctac cgactcgtgg tggaggtctt tggcacctat gtccctggct 300  
acctactcaa gctgagcgcc atgggctggg gcttcccat ctttctggtg 350  
acgctgggtg ccctgggtga tgtggacaac tatggcccca tcatcttggc 400  
tgtgcatagg actccagagg gcgtcatcta cccttccatg tgctggatcc 450  
gggactccct ggtcagctac atcaccaacc tgggcctctt cagcctggtg 500  
tttctgttca acatgg 516

<210> 485

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 485

ggcattggag cagtgctggg tg 22

<210> 486

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 486

tgaggccta gatgcggctg gacg 24 .

<210> 487

<211> 2849

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2715

<223> unknown base

<400> 487

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aagagggctc taggaaaaag ttttgatgg gattatgtgg aaactaccct 150  
gcgattctct gctgccagag caggctcggc gcttccaccc cagtgcagcc 200  
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ccgcggtgag tgagctctca cccagtcag ccaaagagc ctcttcgggc 300  
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gaatccaacc tgagtagtaa attccagttt tccagcaaca aggaacagaa 400  
cggagtacaa gatcctcagc atgagagaat tattactgtg tctactaatg 450  
gaagtattca cagcccaagg tttcctcata cttatccaag aaatacggtc 500  
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gtttgatgaa agatttgggc ttgaagacc agaagatgac atatgcaagt 600  
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tgggtgtggt ctggtactgt accaggaaaa cagatttcta aaggaaatca 700  
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cagtgtccat aagggaagaa ctaaagagaa ccgataccat tttctggcca 1100  
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tcactcaccg acgtggccct ggagcaccat gaggagtgtg actgtgtgtg 1300  
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aaaaaaaaa aaaaaaaaaa aggttttaggg ataacagggt aatgcggcc 2849

<210> 488

<211> 345

<212> PRT

<213> Homo sapiens

<400> 488

Met	Ser	Leu	Phe	Gly	Leu	Leu	Leu	Leu	Thr	Ser	Ala	Leu	Ala	Gly
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Gln	Arg	Gln	Gly	Thr	Gln	Ala	Glu	Ser	Asn	Leu	Ser	Ser	Lys	Phe
				20					25					30
Gln	Phe	Ser	Ser	Asn	Lys	Glu	Gln	Asn	Gly	Val	Gln	Asp	Pro	Gln
				35					40					45
His	Glu	Arg	Ile	Ile	Thr	Val	Ser	Thr	Asn	Gly	Ser	Ile	His	Ser
				50					55					60
Pro	Arg	Phe	Pro	His	Thr	Tyr	Pro	Arg	Asn	Thr	Val	Leu	Val	Trp
				65					70					75
Arg	Leu	Val	Ala	Val	Glu	Glu	Asn	Val	Trp	Ile	Gln	Leu	Thr	Phe
				80					85					90
Asp	Glu	Arg	Phe	Gly	Leu	Glu	Asp	Pro	Glu	Asp	Asp	Ile	Cys	Lys
				95					100					105
Tyr	Asp	Phe	Val	Glu	Val	Glu	Glu	Pro	Ser	Asp	Gly	Thr	Ile	Leu
				110					115					120
Gly	Arg	Trp	Cys	Gly	Ser	Gly	Thr	Val	Pro	Gly	Lys	Gln	Ile	Ser
				125					130					135
Lys	Gly	Asn	Gln	Ile	Arg	Ile	Arg	Phe	Val	Ser	Asp	Glu	Tyr	Phe
				140					145					150
Pro	Ser	Glu	Pro	Gly	Phe	Cys	Ile	His	Tyr	Asn	Ile	Val	Met	Pro
				155					160					165

Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu Pro Pro Ser Ala	170	175	180
Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala Phe Ser Thr	185	190	195
Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp Gln Leu	200	205	210
Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly Lys	215	220	225
Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu	230	235	240
Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe	245	250	255
Ser Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe	260	265	270
Trp Pro Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala	275	280	285
Cys Cys Leu His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys	290	295	300
Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr	305	310	315
Gly Val Arg Gly Leu His Lys Ser Leu Thr Asp Val Ala Leu Glu	320	325	330
His His Glu Glu Cys Asp Cys Val Cys Arg Gly Ser Thr Gly Gly	335	340	345

<210> 489

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 489

acttctcagt gtccataagg g 21

<210> 490

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 490

gaactaaaga gaaccgatac cattttctgg ccaggttgtc 40

<210> 491

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 491

caccacagcg tttaaccagg 20

<210> 492

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 492

acaacaggca cagttccac 20

<210> 493

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 493

ggcggaatcc aacctgagta g 21

<210> 494

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 494

gcggctatcc tcctgtgctc 20

<210> 495

<211> 3283

<212> DNA

<213> Homo sapiens

<400> 495

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gacctctaca ttccattttg gaagaagact aaaaatggtg tttccaatgt 100

ggacactgaa gagacaaatt cttatccttt ttaacataat cctaatttcc 150

aaactccttg gggctagatg gtttcctaaa actctgccct gtgatgtcac 200  
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<210> 496  
 <211> 1049  
 <212> PRT  
 <213> Homo sapiens

<400> 496  
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 Pro Lys Thr Leu Pro Cys Asp Val Thr Leu Asp Val Pro Lys Asn  
 35 40 45  
 His Val Ile Val Asp Cys Thr Asp Lys His Leu Thr Glu Ile Pro  
 50 55 60  
 Gly Gly Ile Pro Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn  
 65 70 75  
 His Ile Pro Asp Ile Ser Pro Ala Ser Phe His Arg Leu Asp His  
 80 85 90  
 Leu Val Glu Ile Asp Phe Arg Cys Asn Cys Val Pro Ile Pro Leu  
 95 100 105  
 Gly Ser Lys Asn Asn Met Cys Ile Lys Arg Leu Gln Ile Lys Pro  
 110 115 120  
 Arg Ser Phe Ser Gly Leu Thr Tyr Leu Lys Ser Leu Tyr Leu Asp  
 125 130 135  
 Gly Asn Gln Leu Leu Glu Ile Pro Gln Gly Leu Pro Pro Ser Leu  
 140 145 150  
 Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile Phe Ser Ile Arg Lys  
 155 160 165  
 Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile Leu Tyr Leu Gly  
 170 175 180  
 Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Tyr Val Ser Tyr Ser Ile  
 185 190 195

Glu Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val Leu Ser	200	205	210
Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Val Leu Pro Ser	215	220	225
Thr Leu Thr Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Lys Ile	230	235	240
Gln Glu Asp Asp Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp	245	250	255
Leu Ser Gly Asn Cys Pro Arg Cys Tyr Asn Ala Pro Phe Pro Cys	260	265	270
Ala Pro Cys Lys Asn Asn Ser Pro Leu Gln Ile Pro Val Asn Ala	275	280	285
Phe Asp Ala Leu Thr Glu Leu Lys Val Leu Arg Leu His Ser Asn	290	295	300
Ser Leu Gln His Val Pro Pro Arg Trp Phe Lys Asn Ile Asn Lys	305	310	315
Leu Gln Glu Leu Asp Leu Ser Gln Asn Phe Leu Ala Lys Glu Ile	320	325	330
Gly Asp Ala Lys Phe Leu His Phe Leu Pro Ser Leu Ile Gln Leu	335	340	345
Asp Leu Ser Phe Asn Phe Glu Leu Gln Val Tyr Arg Ala Ser Met	350	355	360
Asn Leu Ser Gln Ala Phe Ser Ser Leu Lys Ser Leu Lys Ile Leu	365	370	375
Arg Ile Arg Gly Tyr Val Phe Lys Glu Leu Lys Ser Phe Asn Leu	380	385	390
Ser Pro Leu His Asn Leu Gln Asn Leu Glu Val Leu Asp Leu Gly	395	400	405
Thr Asn Phe Ile Lys Ile Ala Asn Leu Ser Met Phe Lys Gln Phe	410	415	420
Lys Arg Leu Lys Val Ile Asp Leu Ser Val Asn Lys Ile Ser Pro	425	430	435
Ser Gly Asp Ser Ser Glu Val Gly Phe Cys Ser Asn Ala Arg Thr	440	445	450
Ser Val Glu Ser Tyr Glu Pro Gln Val Leu Glu Gln Leu His Tyr	455	460	465
Phe Arg Tyr Asp Lys Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys	470	475	480

Glu Ala Ser Phe Met Ser Val Asn Glu Ser Cys Tyr Lys Tyr Gly	485	490	495
Gln Thr Leu Asp Leu Ser Lys Asn Ser Ile Phe Phe Val Lys Ser	500	505	510
Ser Asp Phe Gln His Leu Ser Phe Leu Lys Cys Leu Asn Leu Ser	515	520	525
Gly Asn Leu Ile Ser Gln Thr Leu Asn Gly Ser Glu Phe Gln Pro	530	535	540
Leu Ala Glu Leu Arg Tyr Leu Asp Phe Ser Asn Asn Arg Leu Asp	545	550	555
Leu Leu His Ser Thr Ala Phe Glu Glu Leu His Lys Leu Glu Val	560	565	570
Leu Asp Ile Ser Ser Asn Ser His Tyr Phe Gln Ser Glu Gly Ile	575	580	585
Thr His Met Leu Asn Phe Thr Lys Asn Leu Lys Val Leu Gln Lys	590	595	600
Leu Met Met Asn Asp Asn Asp Ile Ser Ser Ser Thr Ser Arg Thr	605	610	615
Met Glu Ser Glu Ser Leu Arg Thr Leu Glu Phe Arg Gly Asn His	620	625	630
Leu Asp Val Leu Trp Arg Glu Gly Asp Asn Arg Tyr Leu Gln Leu	635	640	645
Phe Lys Asn Leu Leu Lys Leu Glu Glu Leu Asp Ile Ser Lys Asn	650	655	660
Ser Leu Ser Phe Leu Pro Ser Gly Val Phe Asp Gly Met Pro Pro	665	670	675
Asn Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu Lys Ser Phe	680	685	690
Ser Trp Lys Lys Leu Gln Cys Leu Lys Asn Leu Glu Thr Leu Asp	695	700	705
Leu Ser His Asn Gln Leu Thr Thr Val Pro Glu Arg Leu Ser Asn	710	715	720
Cys Ser Arg Ser Leu Lys Asn Leu Ile Leu Lys Asn Asn Gln Ile	725	730	735
Arg Ser Leu Thr Lys Tyr Phe Leu Gln Asp Ala Phe Gln Leu Arg	740	745	750
Tyr Leu Asp Leu Ser Ser Asn Lys Ile Gln Met Ile Gln Lys Thr	755	760	765



Ser Phe Pro Glu Asn Val Leu Asn Asn Leu Lys Met Leu Leu Leu	770	775	780
His His Asn Arg Phe Leu Cys Thr Cys Asp Ala Val Trp Phe Val	785	790	795
Trp Trp Val Asn His Thr Glu Val Thr Ile Pro Tyr Leu Ala Thr	800	805	810
Asp Val Thr Cys Val Gly Pro Gly Ala His Lys Gly Gln Ser Val	815	820	825
Ile Ser Leu Asp Leu Tyr Thr Cys Glu Leu Asp Leu Thr Asn Leu	830	835	840
Ile Leu Phe Ser Leu Ser Ile Ser Val Ser Leu Phe Leu Met Val	845	850	855
Met Met Thr Ala Ser His Leu Tyr Phe Trp Asp Val Trp Tyr Ile	860	865	870
Tyr His Phe Cys Lys Ala Lys Ile Lys Gly Tyr Gln Arg Leu Ile	875	880	885
Ser Pro Asp Cys Cys Tyr Asp Ala Phe Ile Val Tyr Asp Thr Lys	890	895	900
Asp Pro Ala Val Thr Glu Trp Val Leu Ala Glu Leu Val Ala Lys	905	910	915
Leu Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys Leu Glu Glu	920	925	930
Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu Ser Gln	935	940	945
Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Asp Lys	950	955	960
Tyr Ala Lys Thr Glu Asn Phe Lys Ile Ala Phe Tyr Leu Ser His	965	970	975
Gln Arg Leu Met Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe	980	985	990
Leu Glu Lys Pro Phe Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys	995	1000	1005
Arg Leu Cys Gly Ser Ser Val Leu Glu Trp Pro Thr Asn Pro Gln	1010	1015	1020
Ala His Pro Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Ala Thr	1025	1030	1035
Asp Asn His Val Ala Tyr Ser Gln Val Phe Lys Glu Thr Val	1040	1045	

<210> 497  
<211> 4199  
<212> DNA  
<213> Homo sapiens

<400> 497

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<211> 1041

<212> PRT

<213> Homo sapiens

<400> 498

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Ser	Arg	Ser	Tyr	Pro	Cys	Asp	Glu	Lys	Lys	Gln	Asn	Asp	Ser	Val
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Ile	Ala	Glu	Cys	Ser	Asn	Arg	Arg	Leu	Gln	Glu	Val	Pro	Gln	Thr
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Val	Gly	Lys	Tyr	Val	Thr	Glu	Leu	Asp	Leu	Ser	Asp	Asn	Phe	Ile
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Thr	His	Ile	Thr	Asn	Glu	Ser	Phe	Gln	Gly	Leu	Gln	Asn	Leu	Thr
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Lys	Ile	Asn	Leu	Asn	His	Asn	Pro	Asn	Val	Gln	His	Gln	Asn	Gly
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Asn	Pro	Gly	Ile	Gln	Ser	Asn	Gly	Leu	Asn	Ile	Thr	Asp	Gly	Ala
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Phe	Leu	Asn	Leu	Lys	Asn	Leu	Arg	Glu	Leu	Leu	Leu	Glu	Asp	Asn
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Gln	Leu	Pro	Gln	Ile	Pro	Ser	Gly	Leu	Pro	Glu	Ser	Leu	Thr	Glu
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Leu	Ser	Leu	Ile	Gln	Asn	Asn	Ile	Tyr	Asn	Ile	Thr	Lys	Glu	Gly
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Ile	Ser	Arg	Leu	Ile	Asn	Leu	Lys	Asn	Leu	Tyr	Leu	Ala	Trp	Asn
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Cys	Tyr	Phe	Asn	Lys	Val	Cys	Glu	Lys	Thr	Asn	Ile	Glu	Asp	Gly
				185					190					195

Val	Phe	Glu	Thr	Leu	Thr	Asn	Leu	Glu	Leu	Leu	Ser	Leu	Ser	Phe
				200					205					210

Asn	Ser	Leu	Ser	His	Val	Pro	Pro	Lys	Leu	Pro	Ser	Ser	Leu	Arg
				215					220					225

Lys	Leu	Phe	Leu	Ser	Asn	Thr	Gln	Ile	Lys	Tyr	Ile	Ser	Glu	Glu
				230					235					240

Asp Phe Lys Gly	Leu Ile Asn Leu Thr	Leu Leu Asp Leu Ser Gly
245	250	255
Asn Cys Pro Arg	Cys Phe Asn Ala Pro	Phe Pro Cys Val Pro Cys
260	265	270
Asp Gly Gly Ala	Ser Ile Asn Ile Asp	Arg Phe Ala Phe Gln Asn
275	280	285
Leu Thr Gln Leu	Arg Tyr Leu Asn Leu	Ser Ser Thr Ser Leu Arg
290	295	300
Lys Ile Asn Ala	Ala Trp Phe Lys Asn	Met Pro His Leu Lys Val
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Leu Asp Leu Glu	Phe Asn Tyr Leu Val	Gly Glu Ile Val Ser Gly
320	325	330
Ala Phe Leu Thr	Met Leu Pro Arg Leu	Glu Ile Leu Asp Leu Ser
335	340	345
Phe Asn Tyr Ile	Lys Gly Ser Tyr Pro	Gln His Ile Asn Ile Ser
350	355	360
Arg Asn Phe Ser	Lys Leu Leu Ser Leu	Arg Ala Leu His Leu Arg
365	370	375
Gly Tyr Val Phe	Gln Glu Leu Arg Glu	Asp Asp Phe Gln Pro Leu
380	385	390
Met Gln Leu Pro	Asn Leu Ser Thr Ile	Asn Leu Gly Ile Asn Phe
395	400	405
Ile Lys Gln Ile	Asp Phe Lys Leu Phe	Gln Asn Phe Ser Asn Leu
410	415	420
Glu Ile Ile Tyr	Leu Ser Glu Asn Arg	Ile Ser Pro Leu Val Lys
425	430	435
Asp Thr Arg Gln	Ser Tyr Ala Asn Ser	Ser Ser Phe Gln Arg His
440	445	450
Ile Arg Lys Arg	Arg Ser Thr Asp Phe	Glu Phe Asp Pro His Ser
455	460	465
Asn Phe Tyr His	Phe Thr Arg Pro Leu	Ile Lys Pro Gln Cys Ala
470	475	480
Ala Tyr Gly Lys	Ala Leu Asp Leu Ser	Leu Asn Ser Ile Phe Phe
485	490	495
Ile Gly Pro Asn	Gln Phe Glu Asn Leu	Pro Asp Ile Ala Cys Leu
500	505	510
Asn Leu Ser Ala	Asn Ser Asn Ala Gln	Val Leu Ser Gly Thr Glu
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Phe Ser Ala Ile	Pro His Val Lys Tyr	Leu Asp Leu Thr	Asn Asn
530		535	540
Arg Leu Asp Phe	Asp Asn Ala Ser Ala	Leu Thr Glu Leu Ser	Asp
545		550	555
Leu Glu Val Leu	Asp Leu Ser Tyr Asn	Ser His Tyr Phe Arg	Ile
560		565	570
Ala Gly Val Thr	His His Leu Glu Phe	Ile Gln Asn Phe Thr	Asn
575		580	585
Leu Lys Val Leu	Asn Leu Ser His Asn	Asn Ile Tyr Thr Leu Thr	
590		595	600
Asp Lys Tyr Asn	Leu Glu Ser Lys Ser	Leu Val Glu Leu Val	Phe
605		610	615
Ser Gly Asn Arg	Leu Asp Ile Leu Trp	Asn Asp Asp Asp Asn	Arg
620		625	630
Tyr Ile Ser Ile	Phe Lys Gly Leu Lys	Asn Leu Thr Arg Leu	Asp
635		640	645
Leu Ser Leu Asn	Arg Leu Lys His Ile	Pro Asn Glu Ala Phe	Leu
650		655	660
Asn Leu Pro Ala	Ser Leu Thr Glu Leu	His Ile Asn Asp Asn	Met
665		670	675
Leu Lys Phe Phe	Asn Trp Thr Leu Leu	Gln Gln Phe Pro Arg	Leu
680		685	690
Glu Leu Leu Asp	Leu Arg Gly Asn Lys	Leu Leu Phe Leu Thr	Asp
695		700	705
Ser Leu Ser Asp	Phe Thr Ser Ser Leu	Arg Thr Leu Leu Leu	Ser
710		715	720
His Asn Arg Ile	Ser His Leu Pro Ser	Gly Phe Leu Ser Glu	Val
725		730	735
Ser Ser Leu Lys	His Leu Asp Leu Ser	Ser Asn Leu Leu Lys	Thr
740		745	750
Ile Asn Lys Ser	Ala Leu Glu Thr Lys	Thr Thr Thr Lys Leu	Ser
755		760	765
Met Leu Glu Leu	His Gly Asn Pro Phe	Glu Cys Thr Cys Asp	Ile
770		775	780
Gly Asp Phe Arg	Arg Trp Met Asp Glu	His Leu Asn Val Lys	Ile
785		790	795
Pro Arg Leu Val	Asp Val Ile Cys Ala	Ser Pro Gly Asp Gln	Arg
800		805	810

Gly Lys Ser Ile Val Ser Leu Glu Leu Thr Thr Cys Val Ser Asp	815	820	825
Val Thr Ala Val Ile Leu Phe Phe Phe Thr Phe Phe Ile Thr Thr	830	835	840
Met Val Met Leu Ala Ala Leu Ala His His Leu Phe Tyr Trp Asp	845	850	855
Val Trp Phe Ile Tyr Asn Val Cys Leu Ala Lys Val Lys Gly Tyr	860	865	870
Arg Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser	875	880	885
Tyr Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu	890	895	900
Leu Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu	905	910	915
Cys Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp	920	925	930
Asn Leu Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val	935	940	945
Leu Thr Lys Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe	950	955	960
Tyr Leu Ala Leu Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile	965	970	975
Ile Phe Ile Leu Leu Glu Pro Val Leu Gln His Ser Gln Tyr Leu	980	985	990
Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile Leu Gln Trp Pro	995	1000	1005
Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp Gln Thr Leu Arg Asn	1010	1015	1020
Val Val Leu Thr Glu Asn Asp Ser Arg Tyr Asn Asn Met Tyr Val	1025	1030	1035
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<223> Synthetic oligonucleotide probe



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<210> 506

<211> 273

<212> PRT

<213> Homo sapiens

<400> 506

Met	Arg	Gly	Ser	Gln	Glu	Val	Leu	Leu	Met	Trp	Leu	Leu	Val	Leu	1	5	10	15
Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val	20	25	30	
Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val	35	40	45	
Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg	50	55	60	
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	65	70	75	
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	80	85	90	
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	95	100	105	
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro	110	115	120	
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln	125	130	135	
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln	140	145	150	
Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu				

	155		160		165
Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly					
	170		175		180
Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala					
	185		190		195
Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu					
	200		205		210
Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala					
	215		220		225
Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu					
	230		235		240
Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu					
	245		250		255
Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys					
	260		265		270

Lys Asp Ser

<210> 507  
 <211> 1700  
 <212> DNA  
 <213> Homo sapiens

<400> 507  
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<210> 508

<211> 273

<212> PRT

<213> Homo sapiens

<400> 508

Met	Arg	Gly	Ser	Gln	Glu	Val	Leu	Leu	Met	Trp	Leu	Leu	Val	Leu
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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25					30

Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35					40					45

Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg	
				50						55				60	
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	
				65					70					75	
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	
				80					85					90	
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	
				95					100					105	
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro	
				110					115					120	
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln	
				125					130					135	
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln	
				140					145					150	
Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu	
				155					160					165	
Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Pro	Lys	Gly	
				170					175					180	
Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	Asp	Ser	Ala	
				185					190					195	
Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	Leu	Leu	
				200					205					210	
Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala	
				215					220					225	
Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu	
				230					235					240	
Val	His	Ser	Phe	Gln	Gln	Leu	Gly	Arg	Ile	Asp	Ser	Leu	Ser	Glu	
				245					250					255	
Gln	Ile	Ser	Phe	Leu	Glu	Glu	Gln	Leu	Gly	Ser	Cys	Ser	Cys	Lys	
				260					265					270	

Lys Asp Ser

<210> 509

<211> 1538

<212> DNA

<213> Homo sapiens

<400> 509

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gcggccacca tggccacgcc tgggctccag cagcatcagc agcccccagg 200  
accggggagg cacaggtggc cccaccacc cggaggagca gtcctgccc 250  
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<210> 510

<211> 273

<212> PRT

<213> Homo sapiens

<400> 510

Met	Arg	Gly	Ser	Gln	Glu	Val	Leu	Leu	Met	Trp	Leu	Leu	Val	Leu
1				5					10					15

Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25					30

Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35					40					45

Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg
				50					55					60

Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg
				65					70					75

Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro
				80					85					90

Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala
				95					100					105

Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro
				110					115					120

Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln
				125					130					135

Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln
				140					145					150

Arg	Cys	Val	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu
				155					160					165

Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Pro	Lys	Gly
				170					175					180

Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	Asp	Ser	Ala
				185					190					195

Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	Leu	Leu
				200					205					210

Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala
				215					220					225

Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu
				230					235					240



Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu  
245 250 255

Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys  
260 265 270

Lys Asp Ser

<210> 511

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 511

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<210> 512

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 512

ttttccactc ctgtcgggtt gg 22

<210> 513

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 513

ggtgacactt gccagtcaga tgtggatgaa tgcagtgcta ggaggg 46

<210> 514

<211> 2690

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2039-2065

<223> unknown base

<400> 514

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cccgtgggc cggtttatcg ggaggagatt gtcttccagg gctagcaatt 250  
ggacttttga tgatgtttga ccagcggca ggaatagcag gcaacgtgat 300  
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<210> 515

<211> 364

<212> PRT

<213> Homo sapiens

<400> 515

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Lys Leu Pro Gly Arg Asn Thr Phe Cys Cys Asp Gly Arg Val Met

20										25					30				
Met	Ala	Arg	Gln	Lys	Gly	Ile	Phe	Tyr	Leu	Thr	Leu	Phe	Leu	Ile					
				35					40					45					
Leu	Gly	Thr	Cys	Thr	Leu	Phe	Phe	Ala	Phe	Glu	Cys	Arg	Tyr	Leu					
				50					55					60					
Ala	Val	Gln	Leu	Ser	Pro	Ala	Ile	Pro	Val	Phe	Ala	Ala	Met	Leu					
				65					70					75					
Phe	Leu	Phe	Ser	Met	Ala	Thr	Leu	Leu	Arg	Thr	Ser	Phe	Ser	Asp					
				80					85					90					
Pro	Gly	Val	Ile	Pro	Arg	Ala	Leu	Pro	Asp	Glu	Ala	Ala	Phe	Ile					
				95					100					105					
Glu	Met	Glu	Ile	Glu	Ala	Thr	Asn	Gly	Ala	Val	Pro	Gln	Gly	Gln					
				110					115					120					
Arg	Pro	Pro	Pro	Arg	Ile	Lys	Asn	Phe	Gln	Ile	Asn	Asn	Gln	Ile					
				125					130					135					
Val	Lys	Leu	Lys	Tyr	Cys	Tyr	Thr	Cys	Lys	Ile	Phe	Arg	Pro	Pro					
				140					145					150					
Arg	Ala	Ser	His	Cys	Ser	Ile	Cys	Asp	Asn	Cys	Val	Glu	Arg	Phe					
				155					160					165					
Asp	His	His	Cys	Pro	Trp	Val	Gly	Asn	Cys	Val	Gly	Lys	Arg	Asn					
				170					175					180					
Tyr	Arg	Tyr	Phe	Tyr	Leu	Phe	Ile	Leu	Ser	Leu	Ser	Leu	Leu	Thr					
				185					190					195					
Ile	Tyr	Val	Phe	Ala	Phe	Asn	Ile	Val	Tyr	Val	Ala	Leu	Lys	Ser					
				200					205					210					
Leu	Lys	Ile	Gly	Phe	Leu	Glu	Thr	Leu	Lys	Glu	Thr	Pro	Gly	Thr					
				215					220					225					
Val	Leu	Glu	Val	Leu	Ile	Cys	Phe	Phe	Thr	Leu	Trp	Ser	Val	Val					
				230					235					240					
Gly	Leu	Thr	Gly	Phe	His	Thr	Phe	Leu	Val	Ala	Leu	Asn	Gln	Thr					
				245					250					255					
Thr	Asn	Glu	Asp	Ile	Lys	Gly	Ser	Trp	Thr	Gly	Lys	Asn	Arg	Val					
				260					265					270					
Gln	Asn	Pro	Tyr	Ser	His	Gly	Asn	Ile	Val	Lys	Asn	Cys	Cys	Glu					
				275					280					285					
Val	Leu	Cys	Gly	Pro	Leu	Pro	Pro	Ser	Val	Leu	Asp	Arg	Arg	Gly					
				290					295					300					
Ile	Leu	Pro	Leu	Glu	Glu	Ser	Gly	Ser	Arg	Pro	Pro	Ser	Thr	Gln					

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Glu Thr Ser Ser Ser Leu Leu Pro Gln Ser Pro Ala Pro Thr Glu					
	320		325		330
His Leu Asn Ser Asn Glu Met Pro Glu Asp Ser Ser Thr Pro Glu					
	335		340		345
Glu Met Pro Pro Pro Glu Pro Pro Glu Pro Pro Gln Glu Ala Ala					
	350		355		360
Glu Ala Glu Lys					

<210> 516  
 <211> 255  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 36, 38, 88, 118, 135, 193, 213, 222  
 <223> unknown base

<400> 516  
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 cccctgggtg gggaattgtg ttggaaagag gaactaccgc tanttctacc 200  
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 atcgt 255

<210> 517  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 517  
 caacgtgatt tcaaagctgg gctc 24

<210> 518  
 <211> 20  
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<213> Homo sapiens

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<211> 344

<212> PRT

<213> Homo sapiens

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Ser	Glu	Ala	Lys	Gly	Thr	Gly	Val	Pro	Val	Gly	Gln	Lys	Gly	Thr	
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Leu	Gln	Cys	Glu	Ala	Ser	Ala	Val	Pro	Ser	Ala	Glu	Phe	Gln	Trp	
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Tyr	Lys	Asp	Asp	Lys	Arg	Leu	Ile	Glu	Gly	Lys	Lys	Gly	Val	Lys	
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Val	Glu	Asn	Arg	Pro	Phe	Leu	Ser	Lys	Leu	Ile	Phe	Phe	Asn	Val	
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Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala  
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<212> DNA  
<213> Homo sapiens

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<211> 736

<212> PRT

<213> Homo sapiens

<400> 526

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Ser	His	Ser	Thr	Cys	Leu	Thr	Glu	Ala	Cys	Ile	Arg	Val	Ala	Gly		65	70	75
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Glu	Pro	Val	Val	Val	Tyr	Gly	Met	Asp	Tyr	Leu	Gln	Gln	Val	Ser		335	340	345

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Phe Glu Ser Ala Gln Glu Lys Leu Leu Glu Thr Leu Tyr Gly Thr	380	385	390
Lys Lys Ser Cys Val Pro Arg Trp Gln Thr Cys Ile Ser Asn Thr	395	400	405
Asp Asp Ala Leu Gly Phe Ala Leu Gly Ser Leu Phe Val Lys Ala	410	415	420
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Glu Ile Arg Thr Ala Phe Glu Glu Ala Leu Gly Gln Leu Val Trp	440	445	450
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Met Ala Asp Gln Leu Arg Lys Pro Pro Ser Arg Asp Gln Trp Ser	515	520	525
Met Thr Pro Gln Thr Val Asn Ala Tyr Tyr Leu Pro Thr Lys Asn	530	535	540
Glu Ile Val Phe Pro Ala Gly Ile Leu Gln Ala Pro Phe Tyr Ala	545	550	555
Arg Asn His Pro Lys Ala Leu Asn Phe Gly Gly Ile Gly Val Val	560	565	570
Met Gly His Glu Leu Thr His Ala Phe Asp Asp Gln Gly Arg Glu	575	580	585
Tyr Asp Lys Glu Gly Asn Leu Arg Pro Trp Trp Gln Asn Glu Ser	590	595	600
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<210> 527

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<212> DNA

<213> Homo sapiens

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<223> unknown base

<400> 527

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accacccac caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaatc 200  
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cggcgggtgct cctcagcctg tgctgcctgc taccctcctg cctcccggct 400  
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cagcctccag atacagaatg tagatgtgac agatgatggc ccatacacgt 650  
gttctgttca gactcaacat acaccagaa caatgcaggt gcatctaact 700

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<210> 612  
 <211> 352  
 <212> PRT  
 <213> Homo Sapien

<400> 612  
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 Pro Ala Gly Gln Ser Val Asp Phe Pro Trp Ala Ala Val Asp Asn  
 35 40 45  
 Met Met Val Arg Lys Gly Asp Thr Ala Val Leu Arg Cys Tyr Leu  
 50 55 60  
 Glu Asp Gly Ala Ser Lys Gly Ala Trp Leu Asn Arg Ser Ser Ile  
 65 70 75  
 Ile Phe Ala Gly Gly Asp Lys Trp Ser Val Asp Pro Arg Val Ser  
 80 85 90  
 Ile Ser Thr Leu Asn Lys Arg Asp Tyr Ser Leu Gln Ile Gln Asn  
 95 100 105  
 Val Asp Val Thr Asp Asp Gly Pro Tyr Thr Cys Ser Val Gln Thr

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Gln	His	Thr	Pro	Arg	Thr	Met	Gln	Val	His	Leu	Thr	Val	Gln	Val					
				125					130					135					
Pro	Pro	Lys	Ile	Tyr	Asp	Ile	Ser	Asn	Asp	Met	Thr	Val	Asn	Glu					
				140					145					150					
Gly	Thr	Asn	Val	Thr	Leu	Thr	Cys	Leu	Ala	Thr	Gly	Lys	Pro	Glu					
				155					160					165					
Pro	Ser	Ile	Ser	Trp	Arg	His	Ile	Ser	Pro	Ser	Ala	Lys	Pro	Phe					
				170					175					180					
Glu	Asn	Gly	Gln	Tyr	Leu	Asp	Ile	Tyr	Gly	Ile	Thr	Arg	Asp	Gln					
				185					190					195					
Ala	Gly	Glu	Tyr	Glu	Cys	Ser	Ala	Glu	Asn	Ala	Val	Ser	Phe	Pro					
				200					205					210					
Asp	Val	Arg	Lys	Val	Lys	Val	Val	Val	Asn	Phe	Ala	Pro	Thr	Ile					
				215					220					225					
Gln	Glu	Ile	Lys	Ser	Gly	Thr	Val	Thr	Pro	Gly	Arg	Ser	Gly	Leu					
				230					235					240					
Ile	Arg	Cys	Glu	Gly	Ala	Gly	Val	Pro	Pro	Pro	Ala	Phe	Glu	Trp					
				245					250					255					
Tyr	Lys	Gly	Glu	Lys	Lys	Leu	Phe	Asn	Gly	Gln	Gln	Gly	Ile	Ile					
				260					265					270					
Ile	Gln	Asn	Phe	Ser	Thr	Arg	Ser	Ile	Leu	Thr	Val	Thr	Asn	Val					
				275					280					285					
Thr	Gln	Glu	His	Phe	Gly	Asn	Tyr	Thr	Cys	Val	Ala	Ala	Asn	Lys					
				290					295					300					
Leu	Gly	Thr	Thr	Asn	Ala	Ser	Leu	Pro	Leu	Asn	Pro	Pro	Ser	Thr					
				305					310					315					
Ala	Gln	Tyr	Gly	Ile	Thr	Gly	Ser	Ala	Asp	Val	Leu	Phe	Ser	Cys					
				320					325					330					
Trp	Tyr	Leu	Val	Leu	Thr	Leu	Ser	Ser	Phe	Thr	Ser	Ile	Phe	Tyr					
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<210> 613

<211> 1797

<212> DNA

<213> Homo Sapien

<400> 613

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ctgcttttca ccaaattgca atggagcctt tcgaaatcaa tgttccaaag 200  
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aaaactcagt gtccgtcagg attgtcgga gtagtaacc aggccgggct 1400  
gaagtttact acagtgttac ctgggggaca atttgcatg acgagtggca 1450

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 gcgtctgacc cggaaccctt ttactttctc tgctcccgag gtgtcctcgg 1700  
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<210> 614  
 <211> 520  
 <212> PRT  
 <213> Homo Sapien

<400> 614

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Ile	Asn	Val	Pro	Lys	Pro	Lys	Arg	Arg	Asn	Gly	Val	Asn	Phe	Ser	35	40	45	
Leu	Ala	Val	Val	Val	Ile	Tyr	Leu	Ile	Leu	Leu	Thr	Ala	Gly	Ala	50	55	60	
Gly	Leu	Leu	Val	Val	Gln	Val	Leu	Asn	Leu	Gln	Ala	Arg	Leu	Arg	65	70	75	
Val	Leu	Glu	Met	Tyr	Phe	Leu	Asn	Asp	Thr	Leu	Ala	Ala	Glu	Asp	80	85	90	
Ser	Pro	Ser	Phe	Ser	Leu	Leu	Gln	Ser	Ala	His	Pro	Gly	Glu	His	95	100	105	
Leu	Ala	Gln	Gly	Ala	Ser	Arg	Leu	Gln	Val	Leu	Gln	Ala	Gln	Leu	110	115	120	
Thr	Trp	Val	Arg	Val	Ser	His	Glu	His	Leu	Leu	Gln	Arg	Val	Asp	125	130	135	
Asn	Phe	Thr	Gln	Asn	Pro	Gly	Met	Phe	Arg	Ile	Lys	Gly	Glu	Gln	140	145	150	
Gly	Ala	Pro	Gly	Leu	Gln	Gly	His	Lys	Gly	Ala	Met	Gly	Met	Pro	155	160	165	
Gly	Ala	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Ala	Glu	Lys	Gly	Ala	Lys	170	175	180	
Gly	Ala	Met	Gly	Arg	Asp	Gly	Ala	Thr	Gly	Pro	Ser	Gly	Pro	Gln				



185					190					195				
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				200										210
Gly	Ala	Pro	Gly	Lys	Gln	Gly	Ala	Thr	Gly	Thr	Pro	Gly	Pro	Gln
				215										225
Gly	Glu	Lys	Gly	Ser	Lys	Gly	Asp	Gly	Gly	Leu	Ile	Gly	Pro	Lys
				230										240
Gly	Glu	Thr	Gly	Thr	Lys	Gly	Glu	Lys	Gly	Asp	Leu	Gly	Leu	Pro
				245										255
Gly	Ser	Lys	Gly	Asp	Arg	Gly	Met	Lys	Gly	Asp	Ala	Gly	Val	Met
				260										270
Gly	Pro	Pro	Gly	Ala	Gln	Gly	Ser	Lys	Gly	Asp	Phe	Gly	Arg	Pro
				275										285
Gly	Pro	Pro	Gly	Leu	Ala	Gly	Phe	Pro	Gly	Ala	Lys	Gly	Asp	Gln
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Gly	Gln	Pro	Gly	Leu	Gln	Gly	Val	Pro	Gly	Pro	Pro	Gly	Ala	Val
				305										315
Gly	His	Pro	Gly	Ala	Lys	Gly	Glu	Pro	Gly	Ser	Ala	Gly	Ser	Pro
				320										330
Gly	Arg	Ala	Gly	Leu	Pro	Gly	Ser	Pro	Gly	Ser	Pro	Gly	Ala	Thr
				335										345
Gly	Leu	Lys	Gly	Ser	Lys	Gly	Asp	Thr	Gly	Leu	Gln	Gly	Gln	Gln
				350										360
Gly	Arg	Lys	Gly	Glu	Ser	Gly	Val	Pro	Gly	Pro	Ala	Gly	Val	Lys
				365										375
Gly	Glu	Gln	Gly	Ser	Pro	Gly	Leu	Ala	Gly	Pro	Lys	Gly	Ala	Pro
				380										390
Gly	Gln	Ala	Gly	Gln	Lys	Gly	Asp	Gln	Gly	Val	Lys	Gly	Ser	Ser
				395										405
Gly	Glu	Gln	Gly	Val	Lys	Gly	Glu	Lys	Gly	Glu	Arg	Gly	Glu	Asn
				410										420
Ser	Val	Ser	Val	Arg	Ile	Val	Gly	Ser	Ser	Asn	Arg	Gly	Arg	Ala
				425										435
Glu	Val	Tyr	Tyr	Ser	Gly	Thr	Trp	Gly	Thr	Ile	Cys	Asp	Asp	Glu
				440										450
Trp	Gln	Asn	Ser	Asp	Ala	Ile	Val	Phe	Cys	Arg	Met	Leu	Gly	Tyr
				455										465
Ser	Lys	Gly	Arg	Ala	Leu	Tyr	Lys	Val	Gly	Ala	Gly	Thr	Gly	Gln

	470		475		480
Ile Trp Leu Asp Asn Val Gln Cys Arg Gly Thr Glu Ser Thr Leu					
	485		490		495
Trp Ser Cys Thr Lys Asn Ser Trp Gly His His Asp Cys Ser His					
	500		505		510
Glu Glu Asp Ala Gly Val Glu Cys Ser Val					
	515		520		

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 <211> 647  
 <212> DNA  
 <213> Homo Sapien

<400> 615  
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 aaaagccaaa atgaaactga tggctactgt tttcaccatt gggctaactt 200  
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 gttaaacaag tagtaataaa agttaattca atctaaaaaa aaaaaaa 647

<210> 616  
 <211> 98  
 <212> PRT  
 <213> Homo Sapien

<400> 616  
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 20 25 30  
 Lys Ile Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val  
 35 40 45

Ala	Asp	Leu	Thr	Gln	Ile	Asp	Val	Asn	Val	Gln	Asp	His	Phe	Trp
				50					55					60
Asp	Gly	Lys	Gly	Cys	Glu	Met	Ile	Cys	Tyr	Cys	Asn	Phe	Ser	Glu
				65					70					75
Leu	Leu	Cys	Cys	Pro	Lys	Asp	Val	Phe	Phe	Gly	Pro	Lys	Ile	Ser
				80					85					90
Phe	Val	Ile	Pro	Cys	Asn	Asn	Gln							
				95										

<210> 617  
 <211> 2558  
 <212> DNA  
 <213> Homo Sapien

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 accccgccgt ggtggttggg gggcgcgag tagagcagca gcacaggcgc 150  
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cagcaaatga atatgcttat aggcgtggaa ttgcagaggc tggttggtcctt 1050  
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aggcctgggg agaagtgaag agacagattt atgttgcagc cttcacagt 2400



Gly Asn Lys Val	Lys Asn Ala Gln Leu	Ala Gly Ala Lys Gly Val
215	220	225
Ile Leu Tyr Ser	Asp Pro Ala Asp Tyr	Phe Ala Pro Gly Val Lys
230	235	240
Ser Tyr Pro Asp	Gly Trp Asn Leu Pro	Gly Gly Gly Val Gln Arg
245	250	255
Gly Asn Ile Leu	Asn Leu Asn Gly Ala	Gly Asp Pro Leu Thr Pro
260	265	270
Gly Tyr Pro Ala	Asn Glu Tyr Ala Tyr	Arg Arg Gly Ile Ala Glu
275	280	285
Ala Val Gly Leu	Pro Ser Ile Pro Val	His Pro Ile Gly Tyr Tyr
290	295	300
Asp Ala Gln Lys	Leu Leu Glu Lys Met	Gly Gly Ser Ala Pro Pro
305	310	315
Asp Ser Ser Trp	Arg Gly Ser Leu Lys	Val Pro Tyr Asn Val Gly
320	325	330
Pro Gly Phe Thr	Gly Asn Phe Ser Thr	Gln Lys Val Lys Met His
335	340	345
Ile His Ser Thr	Asn Glu Val Thr Arg	Ile Tyr Asn Val Ile Gly
350	355	360
Thr Leu Arg Gly	Ala Val Glu Pro Asp	Arg Tyr Val Ile Leu Gly
365	370	375
Gly His Arg Asp	Ser Trp Val Phe Gly	Gly Ile Asp Pro Gln Ser
380	385	390
Gly Ala Ala Val	Val His Glu Ile Val	Arg Ser Phe Gly Thr Leu
395	400	405
Lys Lys Glu Gly	Trp Arg Pro Arg Arg	Thr Ile Leu Phe Ala Ser
410	415	420
Trp Asp Ala Glu	Glu Phe Gly Leu Leu	Gly Ser Thr Glu Trp Ala
425	430	435
Glu Glu Asn Ser	Arg Leu Leu Gln Glu	Arg Gly Val Ala Tyr Ile
440	445	450
Asn Ala Asp Ser	Ser Ile Glu Gly Asn	Tyr Thr Leu Arg Val Asp
455	460	465
Cys Thr Pro Leu	Met Tyr Ser Leu Val	His Asn Leu Thr Lys Glu
470	475	480
Leu Lys Ser Pro	Asp Glu Gly Phe Glu	Gly Lys Ser Leu Tyr Glu
485	490	495

Ser Trp Thr Lys	Lys Ser Pro Ser Pro	Glu Phe Ser Gly Met	Pro
500		505	510
Arg Ile Ser Lys	Leu Gly Ser Gly Asn	Asp Phe Glu Val	Phe Phe
515		520	525
Gln Arg Leu Gly	Ile Ala Ser Gly Arg	Ala Arg Tyr Thr	Lys Asn
530		535	540
Trp Glu Thr Asn	Lys Phe Ser Gly Tyr	Pro Leu Tyr His	Ser Val
545		550	555
Tyr Glu Thr Tyr	Glu Leu Val Glu Lys	Phe Tyr Asp Pro	Met Phe
560		565	570
Lys Tyr His Leu	Thr Val Ala Gln Val	Arg Gly Gly Met	Val Phe
575		580	585
Glu Leu Ala Asn	Ser Ile Val Leu Pro	Phe Asp Cys Arg	Asp Tyr
590		595	600
Ala Val Val Leu	Arg Lys Tyr Ala Asp	Lys Ile Tyr Ser	Ile Ser
605		610	615
Met Lys His Pro	Gln Glu Met Lys Thr	Tyr Ser Val Ser	Phe Asp
620		625	630
Ser Leu Phe Ser	Ala Val Lys Asn Phe	Thr Glu Ile Ala	Ser Lys
635		640	645
Phe Ser Glu Arg	Leu Gln Asp Phe Asp	Lys Ser Asn Pro	Ile Val
650		655	660
Leu Arg Met Met	Asn Asp Gln Leu Met	Phe Leu Glu Arg	Ala Phe
665		670	675
Ile Asp Pro Leu	Gly Leu Pro Asp Arg	Pro Phe Tyr Arg	His Val
680		685	690
Ile Tyr Ala Pro	Ser Ser His Asn Lys	Tyr Ala Gly Glu	Ser Phe
695		700	705
Pro Gly Ile Tyr	Asp Ala Leu Phe Asp	Ile Glu Ser Lys	Val Asp
710		715	720
Pro Ser Lys Ala	Trp Gly Glu Val Lys	Arg Gln Ile Tyr	Val Ala
725		730	735
Ala Phe Thr Val	Gln Ala Ala Ala Glu	Thr Leu Ser Glu	Val Ala
740		745	750

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